

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/477,484B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 267 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-477-484B-1

Query Match 99.1%; Score 1010; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110; Indels 0; Gaps 0;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFGN 122
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QY 183 YIEGEMRTRIRYNRRS 198
Db 183 YIEGEMRTRIRYNRRS 198
RESULT 9
US-08-646-360-1

;; Sequence 1, Application US/08646360
;; Patent No. 5837491
;; GENERAL INFORMATION:
;; APPLICANT: Better, Marc D.
;; APPLICANT: Carroll, Stephen F.
;; APPLICANT: Studnika, Gary M.
;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 267 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-646-360-1
Query Match 99.1%; Score 1010; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110; Indels 0; Gaps 0;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 123 YDRLEQLAGNLRNIELGNPLEEASALYYSTGCTQPTLARSFIIQIMISEAARFQ 182
QY 183 YIEGEMRTRIRYNRRS 198

Db 183 YIEGEMTRIRYNRRS 198
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RESULT 10
US-08-839-765-1
; Sequence 1, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-765-1
Query Match 99.1%; Score 1010; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 63 SNHAELSVTLALDVTNAYVYVGRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTTAFGNG 122

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QY 183 YIEGEMTRIRYNRRS 198
Db 183 YIEGEMTRIRYNRRS 198
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RESULT 11
US-09-136-389-1
; Sequence 1, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-389-1
Query Match 99.1%; Score 1010; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 123 YDRLEQAGNLRNIELGNPLEEASALYYSTGGTQPLTLARSPFIICQMISEAARFQ 182
QY 183 YIEGEMTRIRYNRRS 198
Db 183 YIEGEMTRIRYNRRS 198

RESULT 12
US-09-610-838-1
; Sequence 1, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-838-1

Query Match 99.1%; Score 1010; DB 4; Length 267;
Best Local Similarity 100.0%; Fred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINQRFILVEL 62
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Db 123 YDRLEQAGNLRNIELGNPLEEASALYYSTGGTQPLTLARSPFIICQMISEAARFQ 182
QY 183 YIEGEMTRIRYNRRS 198
Db 183 YIEGEMTRIRYNRRS 198

RESULT 13
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-09487-1

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Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 123 YDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQLPTLARSFFIICIMISEAARFQ 182
Db 123 YDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQLPTLARSFFIICIMISEAARFQ 182
QY 183 YIEGEMTRIRYNRRS 198
Db 183 YIEGEMTRIRYNRRS 198

RESULT 14
US-08-356-786-8
; Sequence 8, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biotynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-8
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Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 124 YDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQLPTLARSFFIICIMISEAARFQ 182
QY 183 YIEGEMTRIRYNRRS 198
Db 184 YIEGEMTRIRYNRRS 199

RESULT 15
US-08-378-761A-27
; Sequence 27, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-27

Query Match          99.1%; Score 1010; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 1.7e-110;
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Db	207	YIEGEMRTRIRYNRRS	222

Search completed: February 10, 2004, 16:29:33
Job time : 12.4485 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 25.5389 Seconds
(without alignments)
1623.314 Million cell updates/sec

Title: US-10-083-336A-7

Perfect score: 1019

Sequence: 1 MYPKQYPIINTTAGATVQS.....ARFQVIEGMRTRYNRRS 198

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Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 203982283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1019	100.0	198	12	US-10-083-336A-7
2	1019	100.0	267	12	US-10-083-336A-7
3	1019	100.0	267	12	US-10-083-336A-7
4	1010	99.1	198	12	US-10-083-336A-7
5	1010	99.1	199	12	US-10-083-336A-5
6	1010	99.1	200	12	US-10-083-336A-10
7	1010	99.1	267	12	US-10-083-336A-1
8	1010	99.1	576	12	US-10-083-336A-1
9	950	93.2	188	12	US-10-083-336A-8
10	941	92.3	188	12	US-10-083-336A-4
11	941	92.3	189	12	US-10-083-336A-6
12	941	92.3	190	12	US-10-083-336A-11
13	924.5	90.7	185	12	US-10-083-336A-9
14	738	72.4	179	12	US-10-083-336A-2
15	342	33.6	247	10	US-09-792-793A-39

16	342	33.6	247	12	US-10-127-890-6
17	342	33.6	247	12	US-10-375-209A-39
18	342	33.6	289	12	US-10-280-679B-4
19	323.5	31.7	251	12	US-10-282-935-3
20	323.5	31.7	251	12	US-10-440-796-3
21	312	30.6	247	10	US-09-792-793A-34
22	312	30.6	247	12	US-10-375-209A-34
23	279	27.2	263	12	US-10-127-890-4
24	277	27.2	263	12	US-10-127-890-7
25	276	27.1	252	9	US-09-347-064-2
26	276	27.1	252	9	US-09-347-064-8
27	267.5	26.3	248	12	US-10-127-890-5
28	246.5	24.2	251	12	US-10-127-890-110
29	246.5	24.2	251	12	US-10-127-890-111
30	245.5	24.1	251	12	US-10-127-890-101
31	244.5	24.0	251	12	US-10-127-890-99
32	244.5	24.0	251	12	US-10-127-890-107
33	243.5	23.9	251	12	US-10-127-890-100
34	243.5	23.9	251	12	US-10-127-890-106
35	242.5	23.8	251	9	US-09-765-527-247
36	242.5	23.8	251	12	US-10-127-890-2
37	242.5	23.8	251	12	US-10-127-890-102
38	242.5	23.8	251	12	US-10-127-890-103
39	242.5	23.8	251	12	US-10-127-890-104
40	242.5	23.8	251	12	US-10-127-890-105
41	242.5	23.8	316	12	US-10-074-596-1
42	242.5	23.8	507	12	US-10-074-596-11
43	241.5	23.7	251	12	US-10-127-890-109
44	241.5	23.7	293	9	US-09-765-527-259
45	241.5	23.7	309	9	US-09-765-527-253

ALIGNMENTS

RESULT 1

US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US2003018166SAI
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083.336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-7

Query Match	100.0%	Score 1019;	DB 12;	Length 198;
Best Local Similarity	100.0%;	Pred. No. 1.4e-108;		
Matches 198;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	MYPKQYPIINTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFTILV	60	
Db	1	MYPKQYPIINTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFTILV	60	
Qy	61	ELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAPG	120	
Db	61	ELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAPG	120	
Qy	121	GNYDLEQLAGNLRNIEIENGPLEEASALYYSTGTQPTLARSFIICIMSEAR	180	
Db	121	GNYDLEQLAGNLRNIEIENGPLEEASALYYSTGTQPTLARSFIICIMSEAR	180	
Qy	181	FOYIEGMRTRYNRRS	198	

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Db 181 FOYIEGEMTRIRYNRRS 198
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RESULT 2
US-10-282-935-1
; Sequence 1, Application US/10282935
; Publication No. US20030143193A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; FILE REFERENCE: UTSD:884US
; CURRENT APPLICATION NUMBER: US/10/282,935
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-282-935-1

Query Match 100.0%; Score 1019; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.2e-108;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVPKQYPIINFTAGATVQSYTNFIRAVRGRITTTGADVRRHEIPVLPNVRVGLPINQRFILV 60
Db 1 MVPKQYPIINFTAGATVQSYTNFIRAVRGRITTTGADVRRHEIPVLPNVRVGLPINQRFILV 60
Qy 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
Qy 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYVYSTGGTQPLTLARSFIICIMISEAAR 180
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYVYSTGGTQPLTLARSFIICIMISEAAR 180
Qy 181 FOYIEGEMTRIRYNRRS 198
Db 181 FOYIEGEMTRIRYNRRS 198
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US-10-282-935-1

Query Match 100.0%; Score 1019; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.2e-108;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVPKQYPIINFTAGATVQSYTNFIRAVRGRITTTGADVRRHEIPVLPNVRVGLPINQRFILV 60
Db 1 MVPKQYPIINFTAGATVQSYTNFIRAVRGRITTTGADVRRHEIPVLPNVRVGLPINQRFILV 60
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Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
Qy 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYVYSTGGTQPLTLARSFIICIMISEAAR 180
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYVYSTGGTQPLTLARSFIICIMISEAAR 180
Qy 181 FOYIEGEMTRIRYNRRS 198
Db 181 FOYIEGEMTRIRYNRRS 198
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US-10-440-796-1
; Sequence 1, Application US/10440796
; Publication No. US20040009148A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
; FILE REFERENCE: UTSD:603
; CURRENT APPLICATION NUMBER: US/10/440,796
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-3
; Sequence 3, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannenmacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-3

Query Match 99.1%; Score 1010; DB 12; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5e-107;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PKQYPIINFTAGATVQSYTNFIRAVRGRITTTGADVRRHEIPVLPNVRVGLPINQRFILV 62
Db 3 PKQYPIINFTAGATVQSYTNFIRAVRGRITTTGADVRRHEIPVLPNVRVGLPINQRFILV 62
Qy 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122
Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122
Qy 123 YDRLEQLAGNLRENIELGNGLPLEEASALYYVYSTGGTQPLTLARSFIICIMISEAARFQ 182
Db 123 YDRLEQLAGNLRENIELGNGLPLEEASALYYVYSTGGTQPLTLARSFIICIMISEAARFQ 182
Qy 183 YIEGEMTRIRYNRRS 198
Db 183 YIEGEMTRIRYNRRS 198
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RESULT 5

US-10-083-336A-5

; Sequence 5, Application US/10083336A

; Publication No. US20030181665A1

; GENERAL INFORMATION:

; APPLICANT: Olson, Mark A

; APPLICANT: Millard, Charles B

; APPLICANT: Wannemacher, Robert W

; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof

; FILE REFERENCE: P67452US0 (RIID 01-58)

; CURRENT APPLICATION NUMBER: US/10/083,336A

; CURRENT FILING DATE: 2002-05-21

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 199

; TYPE: PRT

; ORGANISM: Ricinus communis

US-10-083-336A-5

Query Match

Best Local Similarity 99.1%; Score 1010; DB 12; Length 199;

Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62

DB 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 63

QY 63 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122

DB 64 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 123

QY 123 YDRLEQLAGNLRNIELGNPLEEBAISALYYSTGTQLTPLARSFIICQIMISEAARFQ 182

DB 124 YDRLEQLAGNLRNIELGNPLEEBAISALYYSTGTQLTPLARSFIICQIMISEAARFQ 183

QY 183 YIEGEMTRIRYNRRS 198

DB 184 YIEGEMTRIRYNRRS 199

RESULT 6

US-10-083-336A-10

; Sequence 10, Application US/10083336A

; Publication No. US20030181665A1

; GENERAL INFORMATION:

; APPLICANT: Olson, Mark A

; APPLICANT: Millard, Charles B

; APPLICANT: Wannemacher, Robert W

; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof

; FILE REFERENCE: P67452US0 (RIID 01-58)

; CURRENT APPLICATION NUMBER: US/10/083,336A

; CURRENT FILING DATE: 2002-05-21

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 200

; TYPE: PRT

; ORGANISM: Ricinus communis

US-10-083-336A-10

Query Match

Best Local Similarity 99.1%; Score 1010; DB 12; Length 200;

Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62

DB 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 63

QY 63 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122

DB 64 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 123

QY 123 YDRLEQLAGNLRNIELGNPLEEBAISALYYSTGTQLTPLARSFIICQIMISEAARFQ 182

DB 124 YDRLEQLAGNLRNIELGNPLEEBAISALYYSTGTQLTPLARSFIICQIMISEAARFQ 183

QY 183 YIEGEMTRIRYNRRS 198

DB 184 YIEGEMTRIRYNRRS 199

RESULT 7

US-10-127-890-1

; Sequence 1, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/127,890

; FILING DATE: 23-Apr-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,360

; FILING DATE: 13-MAY-1996

; APPLICATION NUMBER: PCT/US94/05348

; FILING DATE: 12-MAY-1994

; APPLICATION NUMBER: US 08/064,691

; FILING DATE: 12-MAY-1993

; APPLICATION NUMBER: US 07/988,430

; FILING DATE: 09-DEC-1992

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: McNicholas, Janet M.

; REGISTRATION NUMBER: 32,918

; REFERENCE/DOCKET NUMBER: 200-70.P4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889

; TELEFAX: 312/707-9155

; TELEFAX: 650 388-1248

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 267 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-127-890-1

Query Match

Best Local Similarity 99.1%; Score 1010; DB 12; Length 267;

Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62


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; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match      93.2%; Score 950; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 1.1e-100; Indels 10; Gaps 1;
Matches 188; Conservative 0; Mismatches 0;

Qy 1 MVEPKQPIINFTTAGATVQSYTNFIRAVRGLTTGADVHRHEIPVLPNRVGLPINQRFILV 60
Db 1 MVEPKQPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILV 50

Qy 61 ELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 120
Db 51 ELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 110

Qy 121 GNYDRLEQLAGNLRENIELGNGLPLEEAI S A L Y Y Y S T G T Q L P T L A R S F F I C I Q M I S E A A R 180
Db 111 GNYDRLEQLAGNLRENIELGNGLPLEEAI S A L Y Y Y S T G T Q L P T L A R S F F I C I Q M I S E A A R 170

Qy 181 FOYIEGEMTRIRYNRRS 198
Db 171 FOYIEGEMTRIRYNRRS 188

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RESULT 8

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US-10-083-336A-1
; Sequence 1, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match      99.1%; Score 1010; DB 12; Length 576;
Best Local Similarity 100.0%; Pred. No. 7.1e-107; Indels 0; Gaps 0;
Matches 196; Conservative 0; Mismatches 0;

Qy 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVHRHEIPVLPNRVGLPINQRFILV 62
Db 38 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVHRHEIPVLPNRVGLPINQRFILV 97

Qy 63 SNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 122
Db 98 SNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 157

Qy 123 YDRLEQLAGNLRENIELGNGLPLEEAI S A L Y Y Y S T G T Q L P T L A R S F F I C I Q M I S E A A R F Q 182
Db 158 YDRLEQLAGNLRENIELGNGLPLEEAI S A L Y Y Y S T G T Q L P T L A R S F F I C I Q M I S E A A R F Q 217

Qy 183 YIEGEMTRIRYNRRS 198
Db 218 YIEGEMTRIRYNRRS 233

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RESULT 9

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US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match      93.2%; Score 950; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 1.1e-100; Indels 10; Gaps 1;
Matches 188; Conservative 0; Mismatches 0;

Qy 1 MVEPKQPIINFTTAGATVQSYTNFIRAVRGLTTGADVHRHEIPVLPNRVGLPINQRFILV 60
Db 1 MVEPKQPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILV 50

Qy 61 ELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 120
Db 51 ELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 110

Qy 121 GNYDRLEQLAGNLRENIELGNGLPLEEAI S A L Y Y Y S T G T Q L P T L A R S F F I C I Q M I S E A A R 180
Db 111 GNYDRLEQLAGNLRENIELGNGLPLEEAI S A L Y Y Y S T G T Q L P T L A R S F F I C I Q M I S E A A R 170

Qy 181 FOYIEGEMTRIRYNRRS 198
Db 171 FOYIEGEMTRIRYNRRS 188

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RESULT 10

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US-10-083-336A-4
; Sequence 4, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-4

Query Match      92.3%; Score 941; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 1.2e-99; Indels 10; Gaps 1;
Matches 186; Conservative 0; Mismatches 0;

Qy 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVHRHEIPVLPNRVGLPINQRFILV 62
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILV 52

Qy 63 SNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 122
Db 53 SNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 112

Qy 123 YDRLEQLAGNLRENIELGNGLPLEEAI S A L Y Y Y S T G T Q L P T L A R S F F I C I Q M I S E A A R F Q 182
Db 113 YDRLEQLAGNLRENIELGNGLPLEEAI S A L Y Y Y S T G T Q L P T L A R S F F I C I Q M I S E A A R F Q 172

Qy 183 YIEGEMTRIRYNRRS 198
Db 173 YIEGEMTRIRYNRRS 188

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RESULT 11

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US-10-083-336A-6
; Sequence 6, Application US/10083336A
; Publication No. US20030181665A1

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```
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-6

Query Match          92.3%; Score 941; DB 12; Length 189;
Best Local Similarity 94.9%; Pred. No. 1.2e-99;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PQKYPINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
DB 4 PQKYPINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 53

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122
DB 54 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 113

QY 123 YDRLEQLAGNLRNIELGNGLPLEEBAISALYYSTGTQTLPTLARSFFIICQMISEAARFQ 182
DB 114 YDRLEQLAGNLRNIELGNGLPLEEBAISALYYSTGTQTLPTLARSFFIICQMISEAARFQ 173

QY 183 YIEGEMTRIRYNRRS 198
DB 174 YIEGEMTRIRYNRRS 189

Query Match          92.3%; Score 941; DB 12; Length 190;
Best Local Similarity 94.9%; Pred. No. 1.2e-99;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PQKYPINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
DB 4 PQKYPINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 53

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122
DB 54 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 113

QY 123 YDRLEQLAGNLRNIELGNGLPLEEBAISALYYSTGTQTLPTLARSFFIICQMISEAARFQ 182
DB 114 YDRLEQLAGNLRNIELGNGLPLEEBAISALYYSTGTQTLPTLARSFFIICQMISEAARFQ 173
```

```
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-9

Query Match          90.7%; Score 924.5; DB 12; Length 185;
Best Local Similarity 93.4%; Pred. No. 9e-98;
Matches 183; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 3 PQKYPINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
DB 3 PQKYPINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILVEL 49

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122
DB 50 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 109

QY 123 YDRLEQLAGNLRNIELGNGLPLEEBAISALYYSTGTQTLPTLARSFFIICQMISEAARFQ 182
DB 110 YDRLEQLAGNLRNIELGNGLPLEEBAISALYYSTGTQTLPTLARSFFIICQMISEAARFQ 169

QY 183 YIEGEMTRIRYNRRS 198
DB 170 YIEGEMTRIRYNRRS 185

Query Match          72.4%; Score 738; DB 12; Length 179;
Best Local Similarity 100.0%; Pred. No. 2.2e-76;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
US-10-083-336A-2
; Sequence 2, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-2
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Search completed: February 10, 2004, 16:53:53
Job time : 25.5389 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:35 ; Search time 10.7146 Seconds
(without alignments)
1777.145 Million cell updates/sec

Title: US-10-083-336A-7

Perfect score: 1019

Sequence: 1 MVPKQYPIINFTTAGATVQS.....ARFOYIEGMRTRIRYNRS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: Pirl1:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1010	99.1	576	1 RLCSA	ricin D precursor
2	920.5	90.3	564	1 RLCSA	agglutinin precursor
3	353.5	34.7	528	2 S2431	abrin-d precursor
4	353.5	34.7	562	2 S16022	abrin-c precursor
5	345	33.9	527	2 S32430	abrin-b precursor
6	342	33.6	289	1 RLTTZ	rRNA N-glycosidase
7	338	33.2	247	2 JUT0393	karasurin - Mongol
8	338	33.2	247	2 JCS032	karasurin-B - Tric
9	338	33.2	289	2 JCS606	karasurin C - Tric
10	336.5	33.0	251	2 J39761	abrin (clone 7.2)
11	329.5	32.3	528	1 TLISA	beta-luffin - smoo
12	307.5	30.2	278	2 S23519	luffin-b - smoo
13	300.5	29.5	250	2 JN0108	agglutinin I precu
14	291	28.6	570	2 S62627	agglutinin lectin I
15	286	28.1	254	2 P00018	rRNA N-glycosidase
16	284.5	27.9	277	2 S24494	rRNA N-glycosidase
17	281	27.6	286	2 S25560	rRNA N-glycosidase
18	278	27.3	245	2 J04840	rRNA N-glycosidase
19	277	27.2	286	1 RLPUGG	rRNA N-glycosidase
20	274	26.9	286	2 J04235	rRNA N-glycosidase
21	242.5	23.8	316	2 J07053	rRNA N-glycosidase
22	197.5	19.4	294	2 S28421	rRNA N-glycosidase
23	182	17.9	313	2 S17757	rRNA N-glycosidase
24	180.5	17.7	261	2 JE0401	antiviral protein
25	178	17.5	278	2 A39817	rRNA N-glycosidase
26	156	15.3	272	2 J04811	betavulgin - beet
27	149.5	14.7	289	2 T12573	rRNA N-glycosidase
28	140	13.7	280	1 RLBH	rRNA N-glycosidase
29	137	13.4	275	2 S33631	trititin - wheat

ALIGNMENTS

RESULT 1

RLCSA

ricin D precursor - castor bean

N:Contains: rRNA N-glycosidase (EC 3.2.2.22)

C:Species: Ricinus communis (castor bean)

C>Date: 31-Dec-1993 #sequence-revision 31-Dec-1993 #text change 16-Jul-1999

C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903

R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Jadin, B.F.; Houston, L.L.; Weaver, R.F.

Nucleic Acids Res. 13, 8019-8033, 1985

A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.

A:Reference number: A24041; MUID:86067214; PMID:2999712

A:Accession: A24041

A:Molecule type: DNA

A:Residues: 1-576 <HAL>

A:Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083

R:Tregear, J.W.; Roberts, L.M.

Plant Mol. Biol. 18, 515-525, 1992

A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene

A:Reference number: S20513; MUID:92163016; PMID:1371405

A:Accession: S20513

A:Molecule type: DNA

A:Residues: 1-576 <TRE>

A:Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085

R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.

Eur. J. Biochem. 148, 265-270, 1985

A:Title: Nucleotide sequence of cloned cDNA coding for prepro-ricin.

A:Reference number: A24614; MUID:85179479; PMID:3838723

A:Accession: A24614

A:Molecule type: mRNA

A:Residues: 12-75, 'D', 77-550, 'R', 552-576 <LAM>

A:Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078

R:Yoshitake, S.; Funatsu, G.; Funatsu, M.

Agric. Biol. Chem. 42, 1267-1274, 1978

A:Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile

A:Reference number: A03372

A:Accession: A03372

A:Molecule type: protein

A:Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>

A:Note: this paper cites the others in the series providing experimental details for the

R:Araki, T.; Funatsu, G.

FEBS Lett. 191, 121-124, 1985

A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A:Reference number: A24010

A:Accession: A24010

A:Molecule type: protein

A:Residues: 315-383, 'PS', 386-576 <ARA>

R:Funatsu, G.; Kimura, M.; Funatsu, M.

Agric. Biol. Chem. 43, 2221-2224, 1979

A:Title: Primary structure of Ala chain of ricin D.

A:Reference number: A03374

A:Accession: A03374

A:Molecule type: protein

A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',40527,'E',529-564,'W',566,'H',567-570,'LI',573-574,'P' <FUN>
A;Note: This paper, one of a series, summarizes the experimental details for the determination of the complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
R;Ready, M.P.; Kim, Y.; Robertus, J.D.
Proteins 10, 270-278, 1991
A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of action.
A;Reference number: A48237; PMID:91352006; PMID:1881893
A;Contents: annotation; active site
R;Robertus, J.D.; Robertus, J.D.
Proteins 10, 260-269, 1991
A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A;Reference number: A48238; PMID:91352005; PMID:1881892
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.
Proteins 10, 251-259, 1991
A;Title: Structure of ricin A-chain at 2.5 angstroms.
A;Reference number: A48239; PMID:91352004; PMID:1881891
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which into the cell of the A chain; B chains are also responsible for cell agglutination (lectin).
C;Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subunit.
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-302/Product: ricin D chain A #status experimental <ACH>
F;46-293/Domain: rRNA N-glycosidase homology <RNG>
F;315-576/Product: ricin D chain B #status experimental <BCH>
F;331-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats
F;45,409,449/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;212/Active site: Glu #status experimental
F;215/Active site: Arg #status predicted
F;234-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental
F;336,349,360/Binding site: N-acetylglucosamine (Asp, Gln, Asn) #status experimental
F;548,569/Binding site: N-acetylglucosamine (Asp, Asn) #status experimental

Query Match 99.1%; Score 1010; DB 1; Length 576;
Best Local Similarity 100.0%; Pred. No. 3.6e-93;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PKQYPIINFAGATVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRVGLPINQRFILVEL 62
Db 38 PKQYPIINFAGATVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRVGLPINQRFILVEL 97

Qy 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGN 122
Db 98 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGN 157

Qy 123 YDRLEQAGNLRNIELNGPLERAEISALYYSTGGTQPLTARSFICIQMISEAARFQ 182
Db 158 YDRLEQAGNLRNIELNGPLERAEISALYYSTGGTQPLTARSFICIQMISEAARFQ 217

Qy 183 YIEGEMTRIRYNRRS 198
Db 218 YIEGEMTRIRYNRRS 233

RESULT 2
RLCSAG
agglutinin precursor - castor bean
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A24261; A24210
R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J. Biol. Chem. 260, 15682-15686, 1985
A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
A;Reference number: A24261; PMID:86059449; PMID:2999130
A;Accession: A24261
A;Molecule type: mRNA
A;Residues: 1-564 <ROB>
A;Cross-references: GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701

R;Araki, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
A;Reference number: A24210
A;Accession: A24210
A;Molecule type: protein
A;Residues: 303-325,'F',327-330,'T',332-361,'D',363-373,'G',375-403,'T',405-551,'V',553-557,'E',559-564,'W',566,'H',567-570,'LI',573-574,'P' <FUN>
C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared to ricin.
C;Superfamily: ricin; rRNA N-glycosidase homology
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-290/Product: agglutinin chain A #status predicted <ACH>
F;35-281/Domain: rRNA N-glycosidase homology <RNG>
F;303-564/Product: agglutinin chain B #status experimental <BCH>
F;319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats
F;34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;200,203/Active site: Glu, Arg #status predicted
F;282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
F;324,337,348/Binding site: N-acetylglucosamine (Asp, Gln, Asn) #status predicted
F;397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;536,557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 90.3%; Score 920.5; DB 1; Length 564;
Best Local Similarity 91.8%; Pred. No. 4.1e-75;
Matches 180; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

Qy 3 PKQYPIINFAGATVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRVGLPINQRFILVEL 62
Db 27 PKQYPIINFAGATVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRVGLPINQRFILVEL 86

Qy 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGN 122
Db 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGN 146

Qy 123 YDRLEQAGNLRNIELNGPLERAEISALYYSTGGTQPLTARSFICIQMISEAARFQ 182
Db 147 YDRLEQAGNLRNIELNGPLERAEISALYYSTGGTQPLTARSFICIQMISEAARFQ 205

Qy 183 YIEGEMTRIRYNRRS 198
Db 206 YIEGEMTRIRYNRRS 221

RESULT 3
S3431
abrin-d precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
C;Accession: S3431; S34408
E;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrinins determined by cDNA sequencing. Covalent structure of abrin-d chain A.
A;Reference number: S3429; PMID:93132798; PMID:8421313
A;Accession: S3431
A;Molecule type: mRNA
A;Residues: 1-528 <HUN>
A;Cross-references: GB:M98346
R;Hung, C.; Lee, M.; Lee, T.; Lin, J.
submitted to the EMBL Data Library, March 1993
A;Reference number: S34408
A;Accession: S34408
A;Molecule type: mRNA
A;Residues: 1-169,'C',171-320,'L',322-528 <HU2>
A;Cross-references: GB:M98346
C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p
F;1-251/Product: abrin-d chain A #status predicted <ACH>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;261-528/Product: abrin-d chain B #status predicted <BCH>

F:283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:164,167/Active site: Glu, Arg #status predicted
 F:200,253,361,401,402/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
 F:288,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F:500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 34.7%; Score 353.5; DB 2; Length 528;
 Best Local Similarity 45.5%; Pred. No. 5e-24;
 Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

Qy 5 QYPIINFTAGATVQSYTNFIRAVRGRLTTGADVREHPEIPVLPNRVGLPINORFILVELSN 64
 Db 1 QDQVIFKTEGATQSQYKQFTEALRQLTGG--LIHDPVLPDPPTVEERNRYITVELSN 58
 Qy 65 HAEISVTLALDVNTAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGNYD 124
 Db 59 SERESIEGIDVTNAYVYVAYRAGSQSYEL---RDAPASASTYLPFGTQ-RYSLRFDGSYG 114
 Qy 125 RLEQAGNLRENIELGNGLPEEAISALYYSTGTQTLPTLARSFIIQMISEARFOYI 184
 Db 115 DLERWAHQTRREISGLQALTHAIS---FLRSGASNDEKARTLIVIQMASEARVRYI 171
 Qy 185 EGEKTRIR 193
 Db 172 SNRVGVSR 180

RESULT 4

SL6022
 abrin-c precursor - Indian licorice
 N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Abrus precatorius (Indian licorice)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
 C:Accession: S16022
 R:Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M.
 Eur. J. Biochem. 198, 723-732, 1991
 A:Title: Preproabrin: genomic cloning, characterisation and the expression of the A-chain
 A:Reference number: S16022; MUID:91266957; PMID:2050149
 A:Accession: S16022
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-562 <WOO>
 A:Cross-references: EMBL:X55667; NID:gl6084; PIDN:CAA39202.1; PID:gl6085
 C:Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.
 C:Superfamily: ricin; rRNA N-glycosidase homology
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid
 F:35-285/Product: abrin-c chain A #status predicted <ACH>
 F:41-280/Domain: rRNA N-glycosidase homology <RNG>
 F:295-562/Product: abrin-c chain B #status predicted <BCH>
 F:317-359,360-400,403-441,448-483,487-526,528-562/Region: 40-residue repeats
 F:335/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F:108,147,229,230/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:198,201/Active site: Glu, Arg #status predicted
 F:234,287,395,435,436/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:281-303,320-339,363-380,451-464,490-507/Disulfide bonds: #status predicted
 F:322,346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F:534,555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 34.7%; Score 353.5; DB 2; Length 562;
 Best Local Similarity 45.5%; Pred. No. 5.4e-24;
 Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

Qy 5 QYPIINFTAGATVQSYTNFIRAVRGRLTTGADVREHPEIPVLPNRVGLPINORFILVELSN 64
 Db 35 QDQVIFKTEGATQSQYKQFTEALRQLTGG--LIHDPVLPDPPTVEERNRYITVELSN 92
 Qy 65 HAEISVTLALDVNTAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGNYD 124
 Db 93 SERESIEGIDVTNAYVYVAYRAGSQSYEL---RDAPASASTYLPFGTQ-RYSLRFDGSYG 148

Qy 125 RLEQAGNLRENIELGNGLPEEAISALYYSTGTQTLPTLARSFIIQMISEARFOYI 184
 Db 149 DLERWAHQTRREISGLQALTHAIS---FLRSGASNDEKARTLIVIQMASEARVRYI 205
 Qy 185 EGEKTRIR 193
 Db 206 SNRVGVSR 214

RESULT 5

S32430
 abrin-b precursor - Indian licorice (fragment)
 N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Abrus precatorius (Indian licorice)
 C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
 C:Accession: S32430; JCI399
 R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
 J. Mol. Biol. 229, 263-267, 1993
 A:Title: Primary structure of three distinct isoabrin determined by cDNA sequencing. Cor
 A:Reference number: S32429; MUID:93132798; PMID:8421313
 A:Accession: S32430
 A:Molecule type: mRNA
 A:Residues: 1-527 <HUN>
 A:Cross-references: GB:M98345; NID:gl66296; PIDN:AAA32625.1; PID:gl66297
 R:Kimura, M.; Sumizawa, T.; Funatsu, G.
 Biosci. Biotechnol. Biochem. 57, 166-169, 1993
 A:Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
 A:Reference number: JCI398; MUID:93169023; PMID:7763422
 A:Accession: JCI399

A:Molecule type: protein
 A:Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430,
 A:Experimental source: seed
 C:Superfamily: ricin; rRNA N-glycosidase homology
 C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; py
 F:1-250/Product: abrin-b chain A #status predicted <ACH>
 F:7-245/Domain: rRNA N-glycosidase homology <RNG>
 F:260-527/Product: abrin-b chain B #status experimental <BCH>
 F:282-324,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F:74,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:110,360,400/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:163,166/Active site: Glu, Arg #status predicted
 F:246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted
 F:287,311/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F:499,520/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 33.9%; Score 345; DB 2; Length 527;
 Best Local Similarity 45.5%; Pred. No. 2.9e-23;
 Matches 87; Conservative 22; Mismatches 72; Indels 10; Gaps 4;

Qy 5 QYPIINFTAGATVQSYTNFIRAVRGRLTTGADVREHPEIPVLPNRVGLPINORFILVELSN 64
 Db 1 QDQVIFKTEGATQSQYKQFTEALRQLTGG--LIHGPVLPDPPTLQERNRYISVELSN 58
 Qy 65 HAEISVTLALDVNTAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAGGNYD 124
 Db 59 SDTESIEAGIDVSNAYVYVAYRAGNSYFL---RDAPTSAGSYLFTGTQ-QYSLRFGSYI 114
 Qy 125 RLEQAGNLRENIELGNGLPEEAISALYYSTGTQTLPTLARSFIIQMISEARFOYI 184
 Db 115 DLERLAQTRQQLPLGLQALRHAISFL----QSGTDDQETARTLIVIQMASEARVRYI 170
 Qy 185 EGEKTRIRYN 195
 Db 171 SYRVGVSR 181

RESULT 6

RLT2T
 rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian sr
 N:Alternate names: alpha-TCS; type I ribosome-inactivating protein
 C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)

C>Date: 30-Sep-1988 #sequence revision 26-Jan-1996 #text_change 23-Mar-2001
C/Accession: J0566; A36274; J01093; A36273; J00003
R/Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.
Gene 97, 267-272, 1991
A/Title: Cloning of trichosanthin cDNA and its expression in *Escherichia coli*.
A/Reference number: J0566; MUID:91153657; PMID:1999291
A/Accession: J0566
A/Molecule type: mRNA
A/Residues: 1-289 <SHA>
A/Cross-references: GB:M34858; NID:gl70536; PIDN:AAA34207.1; PID:gl70537
R/Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
J. Biol. Chem. 265, 8670-8674, 1990
A/Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rib
A/Reference number: A36274; MUID:90256790; PMID:2341400
A/Accession: A36274
A/Molecule type: DNA
A/Residues: 1-233, 'T', 235-246, 'M', 248-289 <CHO>
A/Cross-references: GB:J05434; NID:gl70534; PIDN:AAA34206.1; PID:gl70535
R/Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
Acta Genet. Sin. 21, 42-51, 1994
A/Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A/Reference number: J01093; MUID:94271613; PMID:8003348
A/Accession: J01093
A/Molecule type: DNA
A/Residues: 1-72, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <ZHE>
A/Cross-references: GB:S70176; NID:9547148; PIDN:AAB31048.1; PID:9547149
R/Collins, E.J.; Roberts, J.D.; Lopresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
J. Biol. Chem. 265, 8665-8669, 1990
A/Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for ab
A/Reference number: A36273; MUID:90256789; PMID:2341399
A/Accession: A36273
A/Molecule type: protein
A/Residues: 24-270 <COL>
R/Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Pure Appl. Chem. 58, 789-798, 1986
A/Title: Scientific evaluation of Tian Hua Fen (THE): history, chemistry and application
A/Reference number: J00003
A/Accession: J00003
A/Molecule type: protein
A/Residues: 24-56, 'L', 58-59, 'I', 61-71, 'I', 73-81, 85-86, 'L', 88-92, 'DAGLPRAVL', 93-142, 'GL'
R/Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994
A/Reference number: A67091; PDB:1MRJ
A/Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-
R/Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994
A/Reference number: A67092; PDB:1MRK
A/Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24
R/Xiong, J.P.; Xia, Z.X.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, December 1994
A/Reference number: A66711; PDB:1TCS
A/Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
R/Xiong, J.P.; Xia, Z.X.; Wang, Y.
Nat. Struct. Biol. 1, 695-700, 1994
A/Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re
A/Reference number: A58622; MUID:95360714; PMID:7634073
A/Contents: annotation; X-ray crystallography, 1.7 angstroms
C/Comment: Alpha-trichosanthin has been used to induce abortions.
C/Genetics:
A/Genes: tcs
C/Function:
A/Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA ther
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C/Keywords: abortifacient; glycosidase; hydrolase; root; toxin
E:1-23/Domain: signal sequence #status predicted <SIG>
E:24-270/Product: trichosanthin alpha #status experimental <WAT>
E:27-266/Domain: rRNA N-glycosidase homology <RNG>
F:271-289/Domain: carboxyl-terminal propeptide #status predicted <CRP>
F:93,183,186/Active site: Tyr, Glu, Arg #status predicted

Query Match

33.6%; Score 342; DB 1; Length 289;

Best Local Similarity 39.5%; Pred. No. 2.5e-23;
Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps 5;
QY 9 INFTTAGATVQSYTNFIRAVGRLLTTGADVREHPEVLPNVRVGLPINQRFILVELSNHAEL 68
Db 25 VSRLLSGATSSSYGVFISNLKALPNERKL-YDIPLL--RSLPGSQRYALHLTNAYDE 81
QY 69 SVTLALDVTNAYVGYRAGNSAYFFHPDNOEDA-EAITHLFTDVQNRVTFAPGNYDRLE 127
Db 82 TTSVAIDVTNVYIMGYRAGDTSYFF--NEASATEAAKYVFKDAKRVKVTLPYSGNYERLQ 138
QY 128 OLAGNLRNIEIENGNGLEAISALYYSTGGTQLPPLARSFFICIMISEAARFOVIEGE 187
Db 139 TTAAGKIRENIPLGLPALDSAITTLFYNN-----SAASALMVLQISTSEAAKYKFEIQ 193
QY 188 MTRTI 192
Db 194 IGRKV 198
RESULT 7
J00393
karasurin - Mongolian snake-gourd
C/Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
C/Accession: J00393; P50163
R/Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogiwara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A/Title: The complete amino acid sequence of an abortifacient protein, karasurin.
A/Reference number: J00393; MUID:92005921; PMID:1914000
A/Accession: J00393
A/Molecule type: protein
A/Residues: 1-247 <TOI>
A/Note: a sequence which lacks Ala-247 is also shown in this publication
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C/Keywords: abortifacient
F:4-243/Domain: rRNA N-glycosidase homology <RNG>
Query Match 33.2%; Score 338; DB 2; Length 247;
Best Local Similarity 40.0%; Pred. No. 4.7e-23;
Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;
QY 9 INFTTAGATVQSYTNFIRAVGRLLTTGADVREHPEVLPNVRVGLPINQRFILVELSNHAEL 68
Db 2 VSRLLSGATSSSYGVFISNLKALPYERKL-YDIPLL--RSLPGSQRYALHLTNAYDE 58
QY 69 SVTLALDVTNAYVGYRAGNSAYFFHPDNOEDA-EAITHLFTDVQNRVTFAPGNYDRLE 127
Db 59 TTSVAIDVTNVYIMGYRAGDTSYFF--NEASATEAAKYVFKDAKRVKVTLPYSGNYERLQ 115
QY 128 OLAGNLRNIEIENGNGLEAISALYYSTGGTQLPPLARSFFICIMISEAARFOVIEGE 187
Db 116 TTAAGKIRENIPLGLPALDSAITTLFYNN-----SAASALMVLQISTSEAAKYKFEIQ 170
QY 188 MTRTI 192
Db 171 IGRKV 175
RESULT 8
JC5032
karasurin-B - Trichosanthes kirilowii var. japonica
C/Species: Trichosanthes kirilowii var. japonica
C/Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
C/Accession: JC5032
R/Kondo, T.; Mizukami, H.; Takeda, T.; Ogiwara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A/Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
A/Reference number: JC5032; MUID:97108848; PMID:8951169
A/Accession: JC5032
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-247 <KON>

Agric. Biol. Chem. 52, 1095-1097, 1988

J. Mol. Biol. 229, 263-267, 1993
A>Title: Primary structure of three distinct isoforms determined by cDNA sequencing.
A:Reference number: S32429; MUID:93132798; PMID:9421313
A:Accession: S32429
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'E', 2-528 <HUN>
A:Cross-references: GB:M98344; NID:gl66294; PIDN:AAA32624.1; PID:g166295
A>Note: the coding region for the sequence shown is preceded by an ATG codon
A>Note: residues 1-8 were derived from the synthesized primer
R:Funatsu, G.; Taguchi, Y.; Kamenosoro, M.; Yanaka, M.
A:Ar. Biol. Chem. 52, 1095-1097, 1988

QY	9	INFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLNPRVGLPINQRFILVELSNHAEL	68
DB	5	IKFSTEGATQSQYKQFIALRRLRG--LIHDIPLVDPPTLQERNRNVITVELSNSDTE	62
QY	69	SVTLALDVTNAYVVGVRAGNSAYFFH--PDNODAEATHLFTDVQNRVYTFAGGNYDLR	126
DB	63	STEVGLDVTNAYVAVYRAGTQSYFLRDAPSSASD---YLFTGT-DQHSLPFYGTYGDL	116
QY	127	EOLAGNLRNIELGNGLPEEALISALYYSTGTGTQTLARSPILCIOMISEAARFQYIEG	186
DB	117	ERWAHQSRQQIPLGLQALTHGIS---FFRSGDNEEKARTLIVTIQWVAEARFYISN	173
QY	187	EMKTRIR	193
DB	174	RVRVSIQ	180

RESULT 12
 S23519
 beta-luffin - smooth loofah
 C:Species: Luffa cylindrica (smooth loofah)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
 C:Accession: S23519; S23113
 R:Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
 Plant Mol. Biol. 19, 887-889, 1992
 A:Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating
 A:Reference number: S23519; MUID:92353400; PMID:1643290
 A:Accession: S23519
 A:Molecule type: mRNA
 A:Residues: 1-218 <X>
 A:Cross-references: EMBL:X62372; NID:g19149; PIDN:CAA44230.1; PID:g19150
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 F;26-264/Domain: rRNA N-glycosidase homology <RNG>

Query Match	30.2%;	Score	307.5;	DB 2;	Length	278;			
Best Local Similarity	35.8%;	Pred. No.	3.1e-20;						
Matches	67;	Conservative	45;	Mismatches	64;	Indels	11;	Gaps	3;

QY	9	INFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLNPRVGLPINQRFILVELSNHAEL	68
DB	24	VSPSLGADSKSYSKFTALRKALPSKEKVSNIPIILLPSASGA---SRVILMQLSNYDAK	80
QY	69	SVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGNYDLRLEQ	128
DB	81	AITMAIDVTNVYIMGLVNSTSYFF---NESDAKLASQYVFKGSTIVTLTPYSNGYERLQN	137
QY	129	LAGNLRNTELGNGPLEEALISALYYSTGTGTQTLARSPILCIOMISEAARFQYIEGEM	188
DB	138	AACKVREKIPLGFRADFSAITSLFHYDS---TAAAGAFLLVIQTAAERFKYIEGQI	192
QY	189	RTRIRYN	195
DB	193	IERIPKN	199

RESULT 13
 JN0108
 luffin-b - smooth loofah
 C:Species: Luffa cylindrica (smooth loofah)
 C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
 C:Accession: JN0108
 R:Islam, M.R.; Hirayama, H.; Funatsu, G.
 Agric. Biol. Chem. 55, 229-238, 1991
 A:Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from
 A:Reference number: JN0108; MUID:91248488; PMID:1368666
 A:Accession: JN0108
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-250 <ISL>
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 F;5-246/Domain: rRNA N-glycosidase homology <RNG>

Query Match	29.5%;	Score	300.5;	DB 2;	Length	250;
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Best Local Similarity 34.2%; Pred. No. 1.1e-19;
Matches 64; Conservative 48; Mismatches 64; Indels 11; Gaps 3;
QY 9 INFNTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNRRVGLPINQRFILVELSNHAEL 68
DB 3 VSFSLSGADSKSYKSFITALKRPFSEKVNIPULLPSAGA---SRYILMQLSNYDAK 59
QY 69 SVTLALDVNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGNYDRLEQ 128
DB 60 AITMAIDVTNVIMGYLVNSYF---ANESDAKLASQVVFKGSLVTIPYSGNYERLQN 116
QY 129 LAGNLENIEIENGPLEBAISALYYSYTGCTPLTARSFIICIQMISEAARFQVIEGEM 188
DB 117 AAGKIREKIPGLFRALDSALTSIFHYDS-----TAAAAAFVLQTTAAEASRFKIEGQI 171
QY 189 RTRIRYN 195
DB 172 IERIPKN 178
RESULT 14
S62627
agglutinin I precursor - European elder
C:Species: Sambucus nigra (European elder)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C:Accession: S62627; S62619
R:van Damme, E.J.M.; Barre, A.; Rouge, P.; van Leuven, F.; Peumans, W.J.
Eur. J. Biochem. 235, 128-137, 1996
A:Title: The NeuAc(alpha-2,6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A:Reference number: S62619; MUID:96202926; PMID:8631319
A:Accession: S62627
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-570 <VAN>
A:Cross-references: EMBL:U27122; NID:g1141772; PIDN:AAC49158.1; PID:g1141773
A:Accession: S62619
A:Status: preliminary
A:Molecule type: protein
A:Residues: 29-39;309-319 <VA2>
C:Superfamily: ricin; rRNA N-glycosidase homology
F:37-283/Domain: rRNA N-glycosidase homology <RNG>
Query Match 28.6%; Score 291; DB 2; Length 570;
Best Local Similarity 39.0%; Pred. No. 2.4e-18;
Matches 76; Conservative 33; Mismatches 74; Indels 12; Gaps 6;
QY 1 MVPKQVPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNRRVGLPINQRFILV 60
DB 29 VTPPVPSVSFNLTGA--DTYEFELRALQEKVILGNHTAFDLPVLPNPSQVSDSNRFVLV 86
QY 61 ELSNHAELSVTLALDVNAYVGYRAGNSAYFFHPDN--QEDAEATHLFTDVQNRVYTF 118
DB 87 PLNPSGDTVTALDVVNLVAVPSSNGKSVFFSGSTAVQD-----NLFVDT--TQBELN 140
QY 119 FGGNYDRLEQLAGNLENIEIENGPLEBAISALYYS--TGTQPLTARSFIICIQMISE 177
DB 141 FTGNYTSLERQVGRVYIPLGPKSLDQAISSTRTYTLTAGDTKP--IARGLLVVVIQWSE 199
QY 178 AARFQYIEGEMTRI 192
DB 200 AARFRIELRIRTSI 214
RESULT 15
PD0018
mistletoe lectin I A chain - Viscum album (fragment)
C:Species: Viscum album
C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 26-Aug-1999
C:Accession: PD0018
R:Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W.
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
A:Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum album
A:Reference number: PD0018; MUID:98308123; PMID:9642133

A:Accession: PD0018
A:Molecule type: protein
A:Residues: 1-254 <ESC>
C:Superfamily: ricin; rRNA N-glycosidase homology
F:7-246/Domain: rRNA N-glycosidase homology <RNG>
Query Match 28.1%; Score 286; DB 2; Length 254;
Best Local Similarity 38.4%; Pred. No. 2.4e-18;
Matches 81; Conservative 36; Mismatches 56; Indels 38; Gaps 10;
QY 13 TAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNRRVGLPIN--QRFILVELSNHAELSV 70
DB 9 THQTTGEEYFRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNGQDSV 66
QY 71 TLALDVNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGGNYDRLEQLA 130
DB 67 TAAIDVTNAYVAYQAGDQSYFLR-DAPRGAE--THLFTGT--TRSSLPFNGSYDPDLERYA 122
QY 131 GNLENIEIENGPLEBAISALYYSYTGCTPLTARSFIICIQMISEAARF-----Q 182
DB 123 GH-RDQIPLGIDQLIQSVTLARF----PGSTETQARSILILIQMISEAARFNPILWRYRQ 178
QY 183 YIE-----GEMTRIRYN 195
DB 179 YINSGASFLPDVYMLELETSMGQQSTQVQHS 209
Search completed: February 10, 2004, 16:28:02
Job time : 11.7146 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:55 ; Search time 6.60489 Seconds
(without alignments)
1409.756 Million cell updates/sec

Title: US-10-083-336A-7

Perfect score: 1019

Sequence: 1 MYPQYPIINFTTAGATVQS.....ARFQYIEGEMTRIRYNRRS 198

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1010	99.1	576	1	RICI_RICCO
2	920.5	90.3	564	1	AGGL_RICCO
3	353.5	34.7	562	1	ABRC_ABRPR
4	345	33.9	527	1	ABRB_ABRPR
5	342	33.6	289	1	RIP1_TRIKI
6	341.5	33.5	282	1	RIP2_BRYDI
7	338	33.2	289	1	RIPS_TRIKI
8	330.5	32.4	563	1	NIGB_SAMNI
9	329.5	32.3	528	1	ABRA_ABRPR
10	312	30.6	290	1	RIP1_BRYDI
11	300.5	29.5	250	1	RIPB_LUFYC
12	296.5	29.1	286	1	RIP1_CUCFI
13	286	28.1	254	1	MLA_VISAL
14	284.5	27.9	277	1	RIPA_LUFYC
15	281	27.6	286	1	RIP2_MOMBA
16	277	27.2	286	1	RIP1_MOMCH
17	260	25.5	294	1	RIP1_TRIAN
18	242.5	23.8	316	1	RIPG_GELMU
19	197.5	19.4	294	1	RIPA_PHYAM
20	182	17.9	313	1	RIP1_PHYAM
21	180.5	17.7	261	1	RIPS_PHYAM
22	178	17.5	278	1	RIPP_MIRJA
23	140	13.7	280	1	RIP2_HORVU
24	133	13.1	280	1	RIP1_HORVU
25	131	12.9	253	1	RIP7_SAPOF
26	127	12.5	253	1	RIP5_SAPOF
27	124	12.2	299	1	RIP6_SAPOF
28	123.5	12.1	293	1	RIP0_DIACA
29	123	12.1	310	1	RIP2_PHYAM
30	121	11.9	292	1	RIP2_SAPOF
31	111	10.9	319	1	SLTA_BP933
32	110	10.8	236	1	RIP3_SAPOF
33	107	10.5	300	1	RIP3_MAIZE

ALIGNMENTS

RESULT 1

ID	RICI_RICCO	STANDARD;	PRT;	576 AA.
AC	P02879; P02880;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ricin precursor [Contains: Ricin A chain (rRNA N-glycosidase)			
DE	(EC 3.2.2.22); Ricin B chain].			
OS	Ricinus communis (Castor Bean).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid I; Malpighiales; Euphorbiaceae; Ricinus.			
OX	NCBI_TaxID=3988;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067214; PubMed=2999712;			
RA	Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,			
RA	Weaver R.F.;			
RT	"Genomic cloning and characterization of a ricin gene from Ricinus			
RT	communis."			
RL	Nucleic Acids Res. 13:8019-8033(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92163016; PubMed=1371405;			
RA	Tregear J.W., Roberts L.M.;			
RT	"The lectin gene family of Ricinus communis: cloning of a functional			
RT	ricin gene and three lectin pseudogenes."			
RL	Plant Mol. Biol. 18:515-525(1992).			
RN	[3]			
RP	SEQUENCE OF 12-576 FROM N.A.			
RX	MEDLINE=85179479; PubMed=3838723;			
RA	Lamb A., Roberts L.M., Lord J.M.;			
RT	"Nucleotide sequence of cloned cDNA coding for preproricin."			
RL	Eur. J. Biochem. 148:265-270(1985).			
RN	[4]			
RP	SEQUENCE OF 36-302.			
RA	Yoshitake S., Funatsu G., Funatsu M.;			
RT	"Isolation and sequences of peptic peptides, and the complete			
RT	sequence of ile chain of ricin-D."			
RL	Agric. Biol. Chem. 42:1267-1274(1978).			
RN	[5]			
RP	SEQUENCE OF 315-576.			
RA	Funatsu G., Kimura M., Funatsu M.;			
RT	"Primary structure of Ala chain of ricin D.;"			
RL	Agric. Biol. Chem. 43:2221-2224(1979).			
RN	[6]			
RP	CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.			
RX	MEDLINE=90344223; PubMed=1368517;			
RA	Kimura Y., Kusuoku H., Tada M., Takagi S., Funatsu G.;			
RT	"Structural analyses of sugar chains from ricin A-chain variant.;"			
RL	Agric. Biol. Chem. 54:157-162(1990).			
RN	[7]			
RP	REVIEW.			
RX	MEDLINE=21480122; PubMed=11595634;			
RA	Olsnes S., Kozlov J.V.;			

P28522 zea mays (m)
P28892 zea mays (m)
Q00531 hordeum vul
P10149 bacterioph
P08026 bacterioph
O67411 aquifex aeo
O83746 treponema p
P03168 aeromonas p
P75255 mycoplasma
Q06306 aeromonas h
P09167 aeromonas h
P27561 saponaria o

34 105 10.3 301 1 RIPX_MAIZE
35 101.5 10.0 304 1 RIP9_MAIZE
36 99 9.7 560 1 JI60_HORVU
37 90.5 8.9 315 1 SLTA_BP930
38 90 8.8 315 1 SLTA_BP919
39 85.5 8.4 1165 1 SVV_AQUAE
40 85 8.3 609 1 FTSH_TREPA
41 82.5 8.1 492 1 AERA_AERTR
42 81 7.9 305 1 Y348_MYCPN
43 78.5 7.7 485 1 AERS_AERHY
44 78.5 7.7 493 1 AERA_AERHY
45 76 7.5 157 1 RIP4_SAPOF

Query Match 99.1%; Score 1010; DB 1; Length 576;
 Best Local Similarity 100.0%; Pred. No. 1.6e-86;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHEIPVLPNVRGLPINQRFILVEL 62
 DB 38 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHEIPVLPNVRGLPINQRFILVEL 97

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFGNG 122
 DB 98 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFGNG 157

QY 123 YDRLEQAGNLRNENELGNGLPBEAISALYYVSTGQTLPRLARSFIIQMISEARFQ 182
 DB 158 YDRLEQAGNLRNENELGNGLPBEAISALYYVSTGQTLPRLARSFIIQMISEARFQ 217

QY 183 YIEGEMTRIRYNRRS 198
 DB 218 YIEGEMTRIRYNRRS 233

RESULT 2
 AGGL RICCO STANDARD; PRT; 564 AA.
 AC P06750;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain].
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Malpighiales; Euphorbiaceae; Ricinus.
 OX NCBI_TaxID=3988;
 RN [1]
 RP MEDLINE=86059449; PubMed=2999130;
 RA Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
 RT "The primary sequence of Ricinus communis agglutinin. Comparison with ricin.";
 RL J. Biol. Chem. 260:15682-15686(1985).
 RN [2]
 RP SEQUENCE OF 303-564.
 RC TISSUE=Seed;
 RA Araki T., Yoshioka Y., Funatsu G.;
 RT "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds.";
 RL Biochim. Biophys. Acta 872:277-285(1986).
 RN [3]
 RP SEQUENCE OF 303-337.
 RX MEDLINE=80178723; PubMed=6768555;
 RA Lin T.T.-S., Li S.S.-L.;
 RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis.";
 RL Eur. J. Biochem. 105:453-459(1980).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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 CC EMBL; M12089; AAA33869.1; -
 CC EMBL; S40368; AAB22584.1; -

DR PIR; A24261; RLCSAG.
 DR HSSP; P02879; IIR6.
 DR GlycoSuiteDB; P06750; -
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; P003396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; Lectin; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 290 AGGLUTININ A CHAIN.
 FT PROPEP 291 302 LINKER PEPTIDE.
 FT CHAIN 303 564 AGGLUTININ B CHAIN.
 FT DOMAIN 309 436 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 439 563 RICIN B-TYPE LECTIN 2.
 FT REPEAT 319 361 1-ALPHA.
 FT REPEAT 362 402 1-BETA.
 FT REPEAT 405 437 1-GAMMA.
 FT REPEAT 450 485 2-ALPHA.
 FT REPEAT 489 528 2-BETA.
 FT REPEAT 531 558 2-GAMMA.
 FT ACT_SITE 200 200 BY SIMILARITY.
 FT DISULFID 282 306 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 322 341 BY SIMILARITY.
 FT DISULFID 365 382 BY SIMILARITY.
 FT DISULFID 453 466 BY SIMILARITY.
 FT DISULFID 492 509 BY SIMILARITY.
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 337 397 N-LINKED (GLCNAC. .).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. .).
 FT CONFLICT 331 331 F -> T (IN REF. 2).
 FT CONFLICT 362 362 R -> D (IN REF. 2).
 FT CONFLICT 374 374 R -> G (IN REF. 2).
 FT CONFLICT 404 404 R -> T (IN REF. 2).
 FT CONFLICT 552 552 F -> V (IN REF. 2).
 SQ SEQUENCE 564 AA; 62851 MW; D455F2A72F609759 CRC64;

Query Match 90.3%; Score 920.5; DB 1; Length 564;
 Best Local Similarity 91.8%; Pred. No. 3.5e-78;
 Matches 180; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHEIPVLPNVRGLPINQRFILVEL 62
 DB 27 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHEIPVLPNVRGLPINQRFILVEL 86

QY 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFGNG 122
 DB 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFGNG 146

QY 123 YDRLEQAGNLRNENELGNGLPBEAISALYYVSTGQTLPRLARSFIIQMISEARFQ 182
 DB 147 YDRLEQAGNLRNENELGNGLPBEAISALYYVSTGQTLPRLARSFIIQMISEARFQ 205

QY 183 YIEGEMTRIRYNRRS 198
 DB 206 YIEGEMTRIRYNRRS 221

RESULT 3
 ABRIC ABRP STANDARD; PRT; 562 AA.
 ID ABRIC ABRP
 AC P28590;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Abrin-c precursor [Contains: Abrin-c A chain (rRNA N-glycosidase) (EC 3.2.2.22); Abrin-c B chain].
 DE Abrus precatorius (Indian licorice) (Crab's eye).
 OS

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Best Local Similarity 45.5%; Pred.No. 2.4e-25;
Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

QY 5 QYPIINFITAGATVQSYTNFIRAVRGLRTGADVREHPVLNPRVGLPINQRFILVELSN 64
Db 35 QDQVIKFTTEGATSQSYKQFIEALRQLTGG--LIHIDPVLDPDPTTVEERNRYITVELSN 92
QY 65 HAELSVTLDVTNAYVGVYRAGNSAYFFHPDQNOEDAEATHLFTDYONRYTFAFGNYD 124
Db 93 SERESIEVGIDVTNAYVYRAYRAGSQSYEL--RDAPASASTYILPFGTQ-RYSLRFDGSYG 148
QY 125 RLEQLAGNLRENTLGNGLPELEAISALYYSTYGTQTLPRLARSFIIICIMISEAARFYI 184
Db 149 DLERWAHQTRRELSLGLQALTHAIS--FLRSGASNDDEKARTLIVIQVASEAARYYI 205
QY 185 EGEEMTRIR 193
Db 206 SNRVGVSVIR 214

RESULT 4
ABRR_ABRPR STANDARD; PRT; 527 AA.
ID ABRB ABRPR AC Q06077; P81374;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE ABR-b-2003 (Rel. 41, Last annotation update)
DE 28in-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)
DE (EC 3.2.2.22); Abrin-b B chain].
OS Abrus precatorius (indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_Taxid=3816;
XP SEQUENCE FROM N.A.
RP MEDLINE=93132738; PubMed=8421313;
RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
RT "Primary structure of three distinct isoabrin determinants by cDNA
RT sequencing. Conservation and significance.";
RL J. Mol. Biol. 229:263-267(1993).
RN [2]
RP SEQUENCE OF 260-527.
RC TISSUE=Seed;
RC MEDLINE=931169023; PubMed=7763422;
RA Kimura M., Sumizawa T., Funatsu G.;
RA "The complete amino acid sequences of the B-chains of abrin-a and
RT abrin-b, toxic proteins from the seeds of Abrus precatorius.";
RL Biosci. Biotechnol. Biochem. 57:166-169(1993).
CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
CC ABRIN-A IS MORE TOXIC THAN RICIN.
CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
CC PRECEDES ENDOCYTOSIS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC

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DR EMBL, M98345; AAA32625.1; -.
DR FIR, S32430; S32430.
DR HSP, P11140; IABR.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP_1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Pyrrolidone carboxylic acid.
FT CHAIN 1 250 ABRIN-B A CHAIN.
FT PEPTIDE 251 260 LINKER PEPTIDE.
FT CHAIN 261 527 ABRIN-B B CHAIN.
FT DOMAIN 272 399 RICIN B-TYPE LECTIN 1.
FT DOMAIN 402 526 RICIN B-TYPE LECTIN 2.
FT REPEAT 282 324 1-ALPHA.
FT REPEAT 325 365 1-BETA.
FT REPEAT 368 400 1-GAMMA.
FT REPEAT 413 448 2-ALPHA.
FT REPEAT 452 491 2-BETA.
FT REPEAT 494 527 2-GAMMA.
FT ACT_SITE 163 163 BY SIMILARITY.
FT DISULFID 246 268 INTERCHAIN (BY SIMILARITY).
FT DISULFID 285 304 BY SIMILARITY.
FT DISULFID 328 345 BY SIMILARITY.
FT DISULFID 416 429 BY SIMILARITY.
FT DISULFID 455 472 BY SIMILARITY.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 282 282 N -> D (IN REF. 2).
FT CONFLICT 291 291 D -> N (IN REF. 2).
FT CONFLICT 350 351 AE -> PQ (IN REF. 2).
FT CONFLICT 378 378 S -> N (IN REF. 2).
FT CONFLICT 426 426 L -> M (IN REF. 2).
FT CONFLICT 428 428 Y -> D (IN REF. 2).
FT CONFLICT 431 431 N -> D (IN REF. 2).
FT CONFLICT 484 484 R -> K (IN REF. 2).
FT CONFLICT 491 491 N -> Y (IN REF. 2).
FT CONFLICT 493 493 H -> S (IN REF. 2).
FT CONFLICT 502 502 R -> G (IN REF. 2).
FT CONFLICT 509 509 E -> Q (IN REF. 2).
FT CONFLICT 513 513 H -> W (IN REF. 2).
FT CONFLICT 516 516 H -> T (IN REF. 2).
FT SEQUENCE 527 AA; 59114 MW; 3253AB490CE9494A CRC64;
Query Match 33.9%; Score 345; DB 1; Length 527;
Best Local Similarity 45.5%; Pred. No. 1.4e-24;
Matches 87; Conservative 22; Mismatches 72; Indels 10; Gaps 4;
QY 5 QYPLINFTTAGVQSVYTFIRAVRGELTGDVREHVPVLPNVRGLPINQRIILVELSN 64
Db 1 QDVVIFTEGATQSKYKQIEALRDLTG--LIHGIPVLPDPTLQERNRIVSELN 58
QY 65 HAEISVTLADVTNAYVYVGRAGNSAYFFHPDQEDAEATHLFTDVQVRYTFAGGNYD 124
Db 59 SDTESIEAGIDVSNAYVAVRAGNSYEL--RDAPTSASRYLFTGTQ-QYSLRFNGSYI 114
QY 125 RLQOLAGNRENTLGNPLLEEISALYYVSTGTQPLTLARSLFICIMISAAARFQYI 184
Db 115 DLERLARQTRQQIPLGLQALRHAISFL---QSGTDDQEIARTLIIQWASEAARVFI 170
QY 185 EGEWRTIRYN 195
Db 171 SYRVGVSI RTN 181
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RESULT 5

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RIPT_TRIKI
ID RIPT TRIKI STANDARD; PRT; 289 AA.
AC P09989;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribosome-inactivating protein alpha-trichosanthin precursor
DE (tRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Rosidae; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=3677;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Maximowicz;
RX MEDLINE=91153657; PubMed=1999291;
RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
RT "Cloning of trichosanthin cDNA and its expression in Escherichia
coll.>";
RL Gene 97:267-272(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Maximowicz; TISSUE=Leaf;
RX MEDLINE=90256790; PubMed=2341400;
RA Chow T., Feldman R.A., Lovett M., Piatak M.;
RT "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
type I ribosome-inactivating protein.";
RL J. Biol. Chem. 265:8670-8674(1990).
RN [3]
RP SEQUENCE OF 24-270.
RC STRAIN=Maximowicz; TISSUE=Tuberous root;
RX MEDLINE=90256789; PubMed=2341399;
RA Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
Wu P., Hwang K., Piatak M.;
RT "Primary amino acid sequence of alpha-trichosanthin and molecular
models for abrin A-chain and alpha-trichosanthin.";
RL J. Biol. Chem. 265:8665-8669(1990).
RN [4]
RP SEQUENCE OF 24-270.
RC TISSUE=Tuberous root;
RX Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
Tian G.Y., Ni C.Z.;
RT "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
application.";
RL Pure Appl. Chem. 58:789-798(1986).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
RX MEDLINE=94344957; PubMed=8066085;
RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
RT "Structure of trichosanthin at 1.88-A resolution.";
RL Proteins 19:4-13(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RX MEDLINE=95344383; PubMed=7619070;
RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
RT "Studies on crystal structures, active-centre geometry and
dephurinating mechanism of two ribosome-inactivating proteins.";
RL Biochem. J. 309:285-298(1995).
CC -!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION.
CC -!- INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
CC -!- CATALYTIC ACTIVITY: Endohydrolase of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
-----
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or send an email to license@isb-sib.ch).

EMBL; M34859; AAA34207.1; -.	271	289	RIBOSOME-INACTIVATING PROTEIN ALPHA-TRICHOSANTHIN.
EMBL; J05434; AAA34206.1; -.	183	163	MISSING IN MATURE PROTEIN.
PIR; J05666; RUTZ1.	57	60	BY SIMILARITY.
PDB; 1MRJ; 07-FEB-95.	CONFLICT	57	IPLL -> LPLI (IN REF. 4).
PDB; 1MRK; 07-FEB-95.	CONFLICT	82	MISSING (IN REF. 4).
PDB; 1TCS; 10-JUL-95.	CONFLICT	87	I -> L (IN REF. 4).
PDB; 1J4G; 28-JAN-03.	CONFLICT	92	V -> VDAGUPRNAVL (IN REF. 4).
PDB; 1NLI; 21-JAN-03.	CONFLICT	92	K -> S (IN REF. 4).
PDB; IQD2; 24-APR-00.	CONFLICT	143	WS -> LWL (IN REF. 4).
InterPro; IPR001574; RIP.	CONFLICT	144	Q -> T (IN REF. 4).
Pfam; PF00161; RIP; 1.	CONFLICT	196	S -> T (IN REF. 2).
PRINTS; PR00396; SHIGARICIN.	CONFLICT	215	MISSING (IN REF. 4).
PROSITE; PS00275; SHIGA_RICIN; 1.	CONFLICT	231	T -> M (IN REF. 2).
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;	CONFLICT	246	
KW Toxin; Signal; 3D-structure.	CONFLICT	247	
FT SIGNAL	1	23	
FT CHAIN	24	270	
FT FT	271	289	
FT FT	ACT SITE	183	
FT FT	CONFLICT	57	
FT FT	CONFLICT	82	
FT FT	CONFLICT	87	
FT FT	CONFLICT	92	
FT FT	CONFLICT	143	
FT FT	CONFLICT	144	
FT FT	CONFLICT	196	
FT FT	CONFLICT	215	
FT FT	CONFLICT	231	
FT FT	CONFLICT	234	
FT FT	CONFLICT	246	
FT FT	CONFLICT	247	
FT FT	STRAND	25	
FT FT	TURN	30	
FT FT	HELI	34	
FT FT	TURN	47	
FT FT	STRAND	50	
FT FT	TURN	55	
FT FT	STRAND	57	
FT FT	HELI	66	
FT FT	STRAND	70	
FT FT	TURN	78	
FT FT	STRAND	82	
FT FT	TURN	89	
FT FT	STRAND	93	
FT FT	TURN	100	
FT FT	STRAND	102	
FT FT	HELI	109	
FT FT	TURN	115	
FT FT	TURN	120	
FT FT	STRAND	124	
FT FT	HELI	134	
FT FT	TURN	142	
FT FT	HELI	145	
FT FT	STRAND	150	
FT FT	HELI	152	
FT FT	TURN	164	
FT FT	HELI	167	
FT FT	TURN	181	
FT FT	HELI	182	
FT FT	STRAND	187	
FT FT	HELI	188	
FT FT	TURN	196	
FT FT	STRAND	202	
FT FT	HELI	206	
FT FT	TURN	227	
FT FT	STRAND	231	
FT FT	TURN	241	
FT FT	STRAND	245	
FT FT	TURN	251	
FT FT	HELI	254	
FT FT	TURN	259	

FT	STRAND	260	260
FT	STRAND	263	268
FT	TURN	266	268
SQ	SEQUENCE	289 AA; 31676 MW; 5CE09BBG30575BB9 CRC64;	
 Query Match 33.6%; Score 342; DB 1; Length 289; Best Local Similarity 39.5%; Pred. No. 1.2e-24; Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps 5;			
QY	9	INTTTAGATVQSNTNFIRAVGRLLTTCADYVRHEIPVLNRPINORFILVELSNHAEL 68	
Dd	25	VSPFLSGATSSSYGVETISNRKALPNRKLI-YDIPLL--RSSLPGSQRALIHILTNTADE 81	
QY	69	SVTLALDVTNAYVVGYRAGNSAYFFHEDNOEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127	
Dd	82	TISVAIDVTNVINGYRGDTSTIFF---NEASATEAAKYVFKDAMKVLTPLPSGNVERLQ 138	
QY	128	QLAGNIKRENIELNGPLPEBAISALYYSTTGCTOLPTLARSLFIICIMISEARFQYTEGE 187	
Dd	139	TAAKIKRENIPLGLPALDSAITTLFYNNAN-----SAASALMVLIOQTSEAARYKFIEQQ 193	
QY	188	MRTRI 192	
Dd	194	I KRV 198	
 RESULT 6			
RIP2	BYDI	STANDARD;	PRT; 282 AA.
ID	RIP2_BYDI	STANDARD;	PRT; 282 AA.
AC	P98184;-Q9S8J0;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Ribosome-inactivating protein bryodin II precursor (rRNA N-glycosidase) (EC 3.2.2.22) (BD2).		
OS	Bryonia dioica (Red bryony).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid I; Cucurbitales; Cucurbitaceae; Bryonia.		
OX	NCBI_TaxId=3652;		
[1]			
RP	SEQUENCE FROM N.A.		
RA	Siegal C.B., Gawlak S.L., Marquardt H.;		
RT	"Bryodin 2 a ribosome-inactivating protein isolated from the plant Bryonia dioica.";		
RL	Patent number US5597569, 28-JAN-1997.		
[2]			
RP	SEQUENCE OF 22-42.		
RC	TISSUE=Root.		
RX	MEDLINE=95151812; PubMed=7849072;		
RA	Siegal C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,		
RA	Marquardt H.;		
RT	"Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunokonjugates.";		
RL	Bioconj. Chem. 5;423-429(1994).		
CC	-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).		
CC	-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.		
CC	-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.		
CC	TYPE 1 RIP SUBFAMILY.		
CC			
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CC			
DR	EMBL; L34238; -; NOT ANNOTATED_CDS.		
DR	HSP; P09989; 1MRJ.		

DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 DR Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
 KW Multigene family; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 282 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
 FT ACT_SITE 183 183 BY SIMILARITY.
 FT CARBOHYD 25 25 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 282 AA; 30754 MW; C52BE2F6A873769C CRC64;
 Query Match 33.5%; Score 341.5; DB 1; Length 282;
 Best Local Similarity 48.0%; Pred. No. 1.3e-24;
 Matches 86; Conservative 23; Mismatches 57; Indels 13; Gaps 7;
 QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPN-RVGLPINQRFILVELSNHAE 67
 Db 24 INFSLIGATGATVKTIRNLTKLTGTPRVYDIPVLRNAAAGL---ARFQVTLNYNG 80
 QY 68 LSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQVRYTFAGGNYDRLE 127
 Db 81 ESVTVALDVNVVVVAVRAYRAGNTAYFL---ADASTEANNVLFAGI-NHVRLPYGGNYDGLG 136
 QY 128 QLAGNL-RENIELGNGPLREASALVYVSTGGTQPLTARSFIIQIMISEARFOYIE 185
 Db 137 TAGGRISRENIELGFSBISAIQGNFRNP-GTSVP---RAFVITQTVSEARFKYIE 191
 RESULT 7
 RIPS TRIKI
 ID RIPS TRIKI STANDARD; PRT; 289 AA.
 AC P24478;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein karasurin precursor (rRNA
 DE N-glycosidase) (EC 3.2.2.22).
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Root tuber;
 RX MEDLINE=97356562; PubMed=9212998;
 RA Mizukami H., Iida K., Kondo T., Ogihara Y.;
 RT "Cloning and bacterial expression of a gene encoding ribosome-
 RT inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
 RT kirilowii var. japonica."; 713 (1997).
 RL Biol. Pharm. Bull. 20:711-713 (1997).
 RN [2]
 RP SEQUENCE OF 24-270.
 RX MEDLINE=92005921; PubMed=1914000;
 RA Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
 RT "The complete amino acid sequence of an abortifacient protein,
 RT karasurin."; 713 (1997).
 RL Chem. Pharm. Bull. 39:1244-1249 (1991).
 CC -1- FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC
 CC 60S RIBOSOMAL SUBUNITS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; AB000666; BAA21786.1; -.
 DR PIR; JC5606; JC5606.
 DR PIR; JUC393; JUC393.
 DR HSSP; P09989; 1MRJ.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
 KW Toxin; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 270 KARASURIN-C.
 FT CHAIN 24 270 KARASURIN-A.
 FT PROPEP 271 289 REMOVED IN MATURE FORM.
 FT ACT_SITE 183 183 BY SIMILARITY.
 SQ SEQUENCE 289 AA; 31704 MW; 883D3E3242887B26 CRC64;
 Query Match 33.2%; Score 338; DB 1; Length 289;
 Best Local Similarity 40.0%; Pred. No. 2.9e-24;
 Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;
 QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPNVRGLPINQRFILVELSNHAE 68
 Db 25 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALHLTNVADE 81
 QY 69 SVTLALDVTNAVVGVRAGNSAYFFHPDQEDA-EATHLFTDVQVRYTFAGGNYDRLE 127
 Db 82 TISVAIDVTNVVVGVRAGDTSYFF---NEASATEAAKVVFKDAKRVLTPLSYGNYERLQ 138
 QY 128 QLAGNLRENIELGNGPLREASALVYVSTGGTQPLTARSFIIQIMISEARFOYIE 187
 Db 139 IAAGKIRENIPLGLPALDSAITLFFYNNAN-----SAASALMWLIQSTSEAAKYKFEIQ 193
 QY 188 METRI 192
 Db 194 IGRKV 198
 RESULT 8
 NIGB SAMNI
 ID NIGB SAMNI STANDARD; PRT; 563 AA.
 AC P33183; P33184; P93542;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain
 DE (rRNA N-glycosidase) (EC 3.2.2.22); Nigrin b B chain].
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OX NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Bark;
 RX MEDLINE=96215449; PubMed=8647092;
 RA Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
 RT "Characterization and molecular cloning of Sambucus nigra agglutinin V
 RT (nigrin b), a GalNAC-specific type-2 ribosome-inactivating protein
 RT from the bark of elderberry (Sambucus nigra).";
 RL Eur. J. Biochem. 237:505-513 (1996).
 RN [2]
 RP SEQUENCE OF 26-49 AND 298-321.
 RX TISSUE=Bark;
 RX MEDLINE=94003077; PubMed=8400135;
 RA Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,
 RA Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;
 RT "Isolation and partial characterization of nigrin b, a non-toxic
 RT novel type 2 ribosome-inactivating protein from the bark of Sambucus
 RT nigra L.";
 RL Plant Mol. Biol. 22:1181-1186 (1993).
 CC -1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN

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 DR EMBL; M98344; AAA32624.1; ALT INIT.
 DR PIR; S12429; TZLSA.
 DR PDB; IABR; 07-FEB-95.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS02031; RICIN_B_LECTIN; 2.
 DR PROSITE; PS02075; SHIGA_RICIN; 1.
 DR Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.
 FT CHAIN 1 251
 FT ABRIN-A A CHAIN.
 FT LINKER PEPTIDE.
 FT CHAIN 252 261
 FT ABRIN-A B CHAIN.
 FT DOMAIN 262 528
 FT RICIN B-TYPE LECTIN 1.
 FT DOMAIN 273 400
 FT RICIN B-TYPE LECTIN 2.
 FT REPEAT 283 325
 FT 1-ALPHA.
 FT REPEAT 326 366
 FT 1-BETA.
 FT REPEAT 369 401
 FT 1-GAMMA.
 FT REPEAT 414 449
 FT 2-ALPHA.
 FT REPEAT 453 492
 FT 2-BETA.
 FT REPEAT 495 528
 FT 2-GAMMA.
 FT ACT SITE 164 164
 FT BY SIMILARITY.
 FT DISULFID 247 269
 FT INTERCHAIN (BY SIMILARITY).
 FT DISULFID 286 305
 FT BY SIMILARITY.
 FT DISULFID 329 346
 FT BY SIMILARITY.
 FT DISULFID 417 430
 FT BY SIMILARITY.
 FT DISULFID 456 473
 FT BY SIMILARITY.
 FT MOD RES 1 1
 FT PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 361 361
 FT N-LINKED (GLCNAC. .).
 FT CARBOHYD 401 401
 FT N-LINKED (GLCNAC. .).
 FT CONFLICT 202 202
 FT MISSING (IN REF. 2).
 FT CONFLICT 298 298
 FT N -> Y (IN REF. 4).
 FT CONFLICT 427 427
 FT M -> L (IN REF. 4).
 FT CONFLICT 467 467
 FT T -> P (IN REF. 4).
 FT CONFLICT 483 483
 FT V -> L (IN REF. 4).
 FT STRAND 5 8
 FT TURN 10 11
 FT HELIX 14 28
 FT STRAND 32 33
 FT TURN 34 35
 FT STRAND 36 38
 FT TURN 42 43
 FT STRAND 47 49
 FT HELIX 51 57
 FT STRAND 63 69
 FT TURN 70 72
 FT STRAND 75 79
 FT STRAND 83 86
 FT TURN 88 89
 FT TURN 92 93
 FT HELIX 94 97
 FT STRAND 100 101
 FT TURN 103 106
 FT STRAND 113 114
 FT TURN 115 119
 FT HELIX 124 126
 FT STRAND 129 129
 FT TURN 131 142
 FT HELIX 143 144
 FT TURN 148 167
 FT STRAND 168 168
 FT HELIX 169 180
 FT TURN 181 182

FT STRAND 185 185
 FT HELIX 189 196
 FT TURN 197 207
 FT STRAND 212 220
 FT TURN 222 223
 FT STRAND 226 231
 FT TURN 232 233
 FT HELIX 235 239
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 FT TURN 346 348
 FT HELIX 351 353
 FT STRAND 355 355
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 FT STRAND 371 374
 FT TURN 380 381
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 FT STRAND 385 387
 FT HELIX 393 395
 FT STRAND 398 399
 FT STRAND 406 408
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 FT HELIX 417 421
 FT TURN 422 423
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 FT HELIX 435 437
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 FT TURN 450 451
 FT STRAND 452 459
 FT TURN 464 465
 FT STRAND 467 472
 FT TURN 474 475
 FT STRAND 478 480
 FT HELIX 483 484
 FT TURN 486 487
 FT STRAND 490 492
 FT TURN 493 496
 FT STRAND 497 501

Query Match 32.3%; Score 329.5; DB 1; Length 528;
 Best Local Similarity 42.8%; Pred. No. 3.Be-23;
 Matches 80; Conservative 28; Mismatches 66; Indels 13; Gaps 5;

Qy 9 INFTTAGATQSYNTNEIRAVRGRLTTGADYRHEIPVLPNVRVGLPINORFILVELSNEAEL 68
 Db 5 IKFTEGATQSYKQFTEALRRLRGG--LIHDIPLVLPDPTTQQRNRYITVELSNSDTE 62
 Qy 69 SVTLALDVTNAYVVGVRAGNSAYFFH--PDNQEDAEAIHLFTDVQNKRYTFAFGGNDRL 126

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Db 63 SIEGVIDTWAYVAYRAGTQSVFLRDAPSASD-----YLFCT-DQHSLPFYGYGDL 116
QY 127 EQLAGNLRNIELNGPLEEIAISALYYSTGGTOLPTLARSFFICIMISEAARFOYIEG 186
Db 117 ERWAHQSRQIPLGLQALTHGIS---PFRSGGNDNEEKANTLIVIQWVAEAFRIYSN 173
QY 187 EMRTIR 193
Db 174 RVRVSIQ 180

RESULT 10
RIP1_BRYDI
AC P33185; Q9SR19;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
DE (EC 3.2.2.22) (SD1).
OS Bryonia dioica (Red bryony).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Bryonia.
OX NCBI_TaxID=3652;
RN [1]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC TISSUE=Leaf;
RX MEDLINE=97228081; PubMed=9115985;
RA Gawlak S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.,
RA Siegall C.B.;
RT "Molecular, biological, and preliminary structural analysis of
RT recombinant bryodin I, a ribosome-inactivating protein from the plant
RT Bryonia dioica."
RL Biochemistry 36:3095-3103(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Siegall C.B.;
RT "Cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica."
RL Patent number US5541110, 30-JUL-1996.
RN [3]
RP SEQUENCE OF 24-66.
RC TISSUE=Seed;
RX MEDLINE=89326691; PubMed=2753596;
RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
RA Leppl D.;
RT "N-terminal sequence of some ribosome-inactivating proteins."
RL Int. J. Pept. Protein Res. 33:263-267(1989).
RN [4]
RP SEQUENCE OF 24-43.
RC TISSUE=Root;
RX MEDLINE=95151812; PubMed=7849072;
RA Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
RA Marguardt H.;
RT "Characterization of ribosome-inactivating proteins isolated from
RT Bryonia dioica and their utility as carcinoma-reactive
RT immunoconjugates."
RL Bioconj. Chem. 5:423-429(1994).
CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO
CC PRODUCE A SHORTER PROTEIN.
CC -!- BIOTECHNOLOGY: Especially useful as immunotoxin for
CC pharmacological applications as it has low toxicity in rats and
CC mice but is potent once inside target cells.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; I24020; --; NOT_ANNOTATED_CDS.
DR PIR; S16491; S16491.
DR PDB; 1BRY; 04-MAR-98.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KW 3D-structure; Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 270 RIBOSOME-INACTIVATING PROTEIN BRYODIN I.
FT PROPEP 271 290 MISSING IN MATURE PROTEIN.
FT ACT_SITE 183 183 BY SIMILARITY.
FT ACT_SITE 212 212
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN 212 212 E->K: REDUCES ACTIVITY 10-FOLD.
FT CONFLICT 61 65 RSSIS -> LRHXI (IN REF. 3).
FT STRAND 25 28
FT TURN 30 31
FT HELIX 34 46
FT TURN 47 47
FT STRAND 50 54
FT TURN 55 56
FT STRAND 57 60
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FT STRAND 70 76
FT TURN 78 79
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FT TURN 89 92
FT STRAND 93 99
FT TURN 100 101
FT STRAND 102 105
FT HELIX 109 114
FT TURN 115 117
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FT HELIX 167 186
FT STRAND 187 187
FT STRAND 188 196
FT STRAND 202 202
FT HELIX 206 213
FT TURN 214 214
FT HELIX 215 225
FT TURN 226 230
FT STRAND 231 239
FT TURN 241 242
FT STRAND 245 250
FT TURN 251 252
FT HELIX 254 257
FT TURN 258 259
FT STRAND 260 260
FT STRAND 263 263
FT HELIX 266 268
SQ SEQUENCE 290 AA; 31788 MW; E966CD9C031A42DB CRC64;
Query Match 30.6%; Score 312; DB 1; Length 290;
Best Local Similarity 37.3%; Pred. No. 7.7e-22;
Matches 69; Conservative 46; Mismatches 58; Indels 12; Gaps 5;

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QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNPRVGLPINORFILVELSNHAEL 68
DB 25 VSRFUSGATTSYGVFFKNLREALPYERKV-YNIPLL--RSSISGSGRYTLHLHTNYADE 81

QY 69 SVTLALDVNTNAYVVGVRAGNSAYFFHPDNOEDA-EAITHLFTDVQNRVYTFAGGNYDRLE 127
DB 82 TISVAVDVNTVIMGYLAGDVSYFF--NEASATEAAKFVFKDAKKVTLPLPSGNYERLQ 138

QY 128 QLAGNLRNIELNGPLEEASALYYSTGCTQPTLARSFIIQMISEAAARFOYIEGE 187
DB 139 TAAGKIRENIPGLPALDSAITLTYTAS-----SAASALLVLIQSTAESARYKFIHQ 193

QY 188 MRIRYN 192
DB 194 IGRV 198

RESULT 11
RIPB LUFICY STANDARD; PRT; 250 AA.
AC P22851;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
DE (EC 3.2.2.22)
OS Luffa cylindrica (Smooth loofah) (Sponge gourd)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
OX NCBI_TaxID=3670;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=91248488; PubMed=1368666;
RA Islam M.R., Hirayama H., Funatsu G.;
RT "Complete amino acid sequence of luffin-B, a ribosome-inactivating
RT protein from sponge gourd (Luffa cylindrica) seeds.";
RL Agric. Biol. Chem. 65:229-238 (1991).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
DR PIR; JN0108; JN0108.
DR HSSP; P16094; LAHC.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
DR Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin.
FT SIGNAL 1 21
FT CHAIN 22 286
FT ACT_SITE 185 185
FT CARBOHYD 103 103
FT CARBOHYD 110 110
FT CARBOHYD 252 252
SQ SEQUENCE 286 AA; 31771 MW; 4EFD4965604DA1 CRC64;

Query Match 29.5%; Score 300.5; DB 1; Length 250;
Best Local Similarity 34.2%; Pred. No. 7.6e-21;
Matches 64; Conservative 48; Mismatches 64; Indels 11; Gaps 3;

QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNPRVGLPINORFILVELSNHAEL 68
DB 3 VSRFUSGADSKSYKFTALRKALPSKEKVSINPLILPSASGA---SRVILMQLSNYDAK 59

QY 69 SVTLALDVNTNAYVVGVRAGNSAYFFHPDNOEDA-EAITHLFTDVQNRVYTFAGGNYDRLEQ 128
DB 60 AITMAIDVNTVIMGYLVNVTSYF---ANESAKLASQVFKGSTLVITPYSGNVERLQ 116

QY 129 LAGNLRNIELNGPLEEASALYYSTGCTQPTLARSFIIQMISEAAARFOYIEGEM 188
DB 117 AAGKIREKIPGLPALDSALTSTFIHYDS-----TAAAFVLIQTAAEASRKYIEGOI 171

QY 189 MRIRYN 195
DB 172 IERIPKN 178

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RESULT 12
RIP1 CUCFI STANDARD; PRT; 286 AA.
ID RIP1 CUCFI
AC Q9FRX4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
DE (EC 3.2.2.22)
OS Cucumis figareii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=131071;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada T., Ohki S.T., Osaki T.;
RT "Cloning and analysis of a cDNA coding a putative ribosome-
RT inactivating protein from Cucumis figareii.";
RL Plant Biotechnol. 17:337-340 (2000).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB045560; BAB19677.1; -.
DR HSSP; P16094; LAHC.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
DR Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 286
FT ACT_SITE 185 185
FT CARBOHYD 103 103
FT CARBOHYD 110 110
FT CARBOHYD 252 252
SQ SEQUENCE 286 AA; 31771 MW; 4EFD4965604DA1 CRC64;

Query Match 29.1%; Score 296.5; DB 1; Length 286;
Best Local Similarity 34.4%; Pred. No. 2.1e-20;
Matches 65; Conservative 47; Mismatches 64; Indels 13; Gaps 5;

QY 9 INFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNPRVGLPINORFILVELSNHAEL 67
DB 28 VKFSLGSGNHSKSYKFTSMNALPNAGDI-YNIPLLVPSISG---SRVILMQLSNYEG 83

QY 68 LSVTALDVNTNAYVVGVRAGNSAYFFHPDNOEDA-EAITHLFTDVQNRVYTFAGGNYDRLE 127
DB 84 NITMAVDVNTVIMGYLVNVTSYF---NETDAQASKFVFGTKSTLTPSYGNYQKLIQ 140

QY 128 QLAGNLRNIELNGPLEEASALYYSTGCTQPTLARSFIIQMISEAAARFOYIEGE 187
DB 141 SVARKERDSIPLGFALDSALTSTLYYDSRAPI-----AFLVLIQTAAEARYKIEKQ 195

QY 188 MRIRYN 196
DB 196 IIRISVSK 204

RESULT 13

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MLA_VISAL STANDARD; PRT; 254 AA.

AC P81446;

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Beta-galactoside specific lectin I A chain (MLA) (ML-I A) (rRNA N-glycosidase) (EC 3.2.2.22).

DE Viscum album (European mistletoe).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Magnoliophyta; eudicotyledons; core eudicots; Santalales; Santalaceae; Viscum.

NCBI_TaxID=3972;

[1]

SEQUENCE.

RC STRAIN=Subsp. album;

RC MEDLINE=97134581; PubMed=8980141;

RA Soler M.H., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T., Voelter W.;

RL "Complete amino acid sequence of the A chain of mistletoe lectin I.";

RL FEBS Lett. 399:153-157(1996).

CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY INTO THE CELL OF THE A CHAIN. B CHAINS ARE ALSO RESPONSIBLE FOR CELL AGGLUTINATION (LECTIN ACTIVITY).

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -!- SUBUNIT: Disulfide-linked dimer of A and B chains.

CC -!- PHARMACEUTICAL: Due to its immunomodulative effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid tumors.

CC -!- MISCELLANEOUS: TWO ISOPRFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA AND NON-GLYCOSYLATED FORM MLA.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC TYPE 2 RIP SUBFAMILY.

DR PIR; PD0018; IABR.

DR HSSP; P11140; IABR.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA_RICIN; FALSE NEG.

KW Plant defense; Hydrolase; Toxin; Repeat; Glycoprotein; Lectin.

FT ACT_SITE 165 165 BY SIMILARITY

FT CAREORD 112 112 N-LINKED (GLCNAC. . .).

FT VARIANT 15 15 E -> D (IN MLA').

FT VARIANT 66 66 V -> I (IN MLA').

FT VARIANT 112 112 N -> T (IN MLA').

FT VARIANT 116 116 P -> T (IN MLA').

FT VARIANT 133 134 DQ -> EE (IN MLA').

FT VARIANT 140 140 T -> S (IN MLA').

FT VARIANT 144 144 F -> Y (IN MLA').

FT VARIANT 151 151 T -> A (IN MLA').

FT VARIANT 179 179 Y -> D (IN MLA').

FT VARIANT 184 184 A -> E (IN MLA').

FT VARIANT 190 190 V -> M (IN MLA').

FT VARIANT 218 218 I -> F (IN MLA').

FT VARIANT 223 224 PP -> ST (IN MLA').

FT VARIANT 231 231 T -> S (IN MLA').

FT VARIANT 235 235 D -> S (IN MLA').

SQ SEQUENCE 254 AA; 28478 MW; 53BAF98D3E0FFE67 CRC64;

Query Match 28.1%; Score 286; DB 1; Length 254;

Best Local Similarity 38.4%; Pred. No. 1.7e-19;

Matches 81; Conservative 36; Mismatches 56; Indels 38; Gaps 10;

QY 13 TAGATGQSYNTFRAVGRGLTTGADVRHEIPVLPNVRVGLPIN--QRFLVELSNHAEISV 70

DB 9 THQTTGEYFRITLLRDYVSSGS-PSNEIFLL-RQSITPVSDAQRFLVELTNGQDSV 66

QY 71 TLALDVTNAYVGVYRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGGNYDRLEQIA 130

Db 67 TAAIDVTNAYVAYAGDQSYFLR-DAPRGAE--THLFTGT-TRSLPFGNSYDPLERVA 122

QY 131 GNLRNIEIENGPLEEALYSALYYSTGGTQLTPLTARSFICIMISEAARF-----Q 182

Db 123 GH-RDQIPLGIDLIQSVTALRF---PGGSTRQARSILLIOMISEAARFNFILWRYRQ 178

QY 183 YIE-----GEMRTIRYN 195

Db 179 YINGSGASFPLDVYMLELETSGWQQSTQVQHS 209

RESULT 14

RIPA_LUFUCY STANDARD; PRT; 277 AA.

AC Q00465;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribosome-inactivating protein luffin-alpha precursor (rRNA N-glycosidase) (EC 3.2.2.22).

OS Luffia cylindrica (Smooth loofah) (Sponge gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Luffa.

NCBI_TaxID=3670;

[1]

SEQUENCE FROM N.A.

RP TISSUE=Seed;

RC MEDLINE=92288316; PubMed=1600156;

RA Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.;

RT "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein from Luffia cylindrica.";

RL Plant Mol. Biol. 18:1199-1202(1992).

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC TYPE 1 RIP SUBFAMILY.

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CC EMBL; X62371; CAA44229.1; .

DR PIR; S22494; S22494.

DR HSSP; P16094; IABC.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA_RICIN; 1.

KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase; Toxin; Signal.

FT SIGNAL 1 19 RIBOSOME-INACTIVATING PROTEIN LUFFIN-ALPHA.

FT CHAIN 20 277

FT ACT_SITE 179 179 BY SIMILARITY.

SQ SEQUENCE 277 AA; 30212 MW; EAL7FC27998C25AC CRC64;

Query Match 27.9%; Score 284.5; DB 1; Length 277;

Best Local Similarity 33.5%; Pred. No. 2.7e-19;

Matches 63; Conservative 45; Mismatches 69; Indels 11; Gaps 3;

QY 9 INFATTAGTQSYNTFRAVGRGLTTGADVRHEIPVLPNVRVGLPINORFILVELSNHAEI 68

Db 22 VRFSLSSGSSSTYSKFGIDLRKALPSNGTVNYITLLSSASGA---SRYTLMTLSNDGK 78

QY 69 SVTLALDVTNAYVGVYRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGGNYDRLEQ 128

Db 79 AITVADVNTVNYIMGVNLTSTSYFF---NESDAKLASQYVFKGSTIVTLPSYGNIEKLT 135

QY 129 LAGNLENIELNGPLEEALISALYYSTGGTOLPTLARSFIICIQMISEAARFQVIEGEM 188
Db 136 AAGKIREKIPDGFPALDSAITLLEHYDS-----TAAAFVILIIQTAAASRFKIEGQI 190
QY 189 RTRIRYNR 196
Db 191 IERISKQ 198

RESULT 15
ID RIP2 MOMBA STANDARD; PRT; 286 AA.
AC P29339;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribosome-inactivating protein momordin II precursor (rRNA N-glycosidase) (EC 3.2.2.22).
OS Momordica balsamina (Bitter melon)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
OX NCBI_TaxID=3672;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=93027170; PubMed=1408771;
RT Ortigao M., Better M.;
RT "Momordin II, a ribosome inactivating protein from Momordica
RT balsamina, is homologous to other plant proteins.";
RT Nucleic Acids Res. 20:4662-4662(1992).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z12175; CAA78166.1; -.
DR PIR; S25560; S25560.
DR FDB; 1CF5; 07-JUN-99.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
FT 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 286 RIBOSOME-INACTIVATING PROTEIN MOMORDIN
FT II.
FT ACT_SITE 181 181 BY SIMILARITY.
FT FT
SQ SEQUENCE 286 AA; 32031 MW; 3B897F1AE6B25986 CRC64;
Query Match 27.6%; Score 281; DB 1; Length 286;
Best Local Similarity 35.1%; Pred. No. 5.9e-19;
Matches 68; Conservative 42; Mismatches 72; Indels 12; Gaps 5;
QY 2 VPKQYPIINFTAGATVQSYTNFIRAVRGLTGTADVRHEIPVLPNVRGLPINQRPILVE 61
Db 18 VPTAKGVNFDLSTAKTYTKFIEDFRATLPFSHKV-YDIPLLXSTIS--DSRRFILLID 74
QY 62 LSNHRELSTLALDVNAVGVGRAGNSAYFEHPDQEDAEALHTLFTDVQNYTFACGG 121
Db 75 LTIYAYETISVALDVNTVNAVYTRDVSFF--KESPEAYNILFKGTR-KITLPYTG 130
QY 122 NYDRLEQLAGNLENIELNGPLEEALISALYYSTGGTOLPTLARSFIICIQMISEAARF 181

Db 131 NYENLQTAHAKIRENIDLGLPALSAITTLFYNA-----QSAPSAALLVLQTTAAARF 185
QY 182 QYIEGEMFTRIRYN 195
Db 186 KYIERHVAKYVATN 199

Search completed: February 10, 2004, 16:23:24
Job time : 6.60489 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:00 ; Search time 26.4196 Seconds
(without alignments)
1933.961 Million cell updates/sec

Title: US-10-083-336A-7

Perfect score: 1019
Sequence: 1 MVPKQYPIINTAGATVQS.....ARFQYIEGEMTRINYNRS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	98.8	541	10 Q41174	Q41174 ricinus com
2	401.5	39.4	580	10 Q94BW3	Q94BW3 cinnamomum
3	397.5	39.0	580	10 Q94BW4	Q94BW4 cinnamomum
4	397.5	39.0	581	10 Q94BW5	Q94BW5 cinnamomum
5	395.5	38.8	549	10 Q9FV22	Q9FV22 cinnamomum
6	350.5	34.4	563	10 O04367	O04367 sambucus ni
7	347.5	34.1	564	10 Q9AVR2	Q9AVR2 sambucus eb
8	344.5	33.8	528	10 Q06076	Q06076 abrus preca
9	340	33.4	289	10 Q94KE4	Q94KE4 trichosanthe
10	338	33.2	247	10 Q9LRE3	Q9LRE3 trichosanthe
11	338	33.2	289	10 Q41216	Q41216 trichosanthe
12	336.5	33.0	252	10 Q38760	Q38760 abrus preca
13	330.5	32.4	563	10 Q945S2	Q945S2 sambucus ni
14	330.5	32.4	563	10 Q8GT32	Q8GT32 sambucus ni
15	329.5	32.3	252	10 Q38761	Q38761 abrus preca
16	324	31.8	270	10 Q8LPV7	Q8LPV7 trichosanthe

RESULT 1

Q41174	PRELIMINARY;	PRT;	541 AA.
ID	Q41174		
AC	Q41174;		
DT	01-NOV-1996 (TRENBLrel. 01, Created)		
DT	01-NOV-1996 (TRENBLrel. 01, Last sequence update)		
DE	01-MAR-2003 (TRENBLrel. 23, Last annotation update)		
DE	Protein A chain (EC 3.2.2.22) (rRNA N-glycosidase)		
DE	(Fragment).		
OS	Ricinus communis (Castor bean).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid 1; Malpighiales; Euphorbiaceae; Ricinus.		
OX	NCBI_TaxID=3988;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92338377; PubMed=1633311;		
RA	Roberts L.M., Tregear J.W., Lord J.M.;		
RT	"Molecular cloning of ricin.;"		
RT	Targeted diagn. Ther. 7:81-97(1992).		
CC	!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.		
CC	!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.		
DR	EMBL; S40366; A822382.1; -		
DR	HSSP; P02879; 1BR6.		
DR	InterPro; IPR000772; Ricin_B_lectin.		
DR	InterPro; IPR001574; RIP.		
DR	InterPro; IPR001400; Somatotropin.		
DR	Pfam; PF00652; Ricin_B_lectin; 6.		
DR	Pfam; PF00161; RIP; 1.		
DR	PRINTS; P000396; SHIGARICIN.		
DR	SMART; SM00458; RICIN; 2.		
DR	PROSITE; PS00231; RICIN_B_LECTIN; 2.		
DR	PROSITE; PS00275; SHIGA_RICIN; 1.		
DR	PROSITE; PS00338; SOMATOTROPIN_2; 1.		
DR	HydroLase; Toxin.		
FT	NON TER		
FT	SEQUENCE 541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;		
SQ			

ALIGNMENTS

Q96236 abrus preca
Q96237 abrus preca
Q04071 sambucus ni
Q41611 trichosanthe
Q96235 abrus preca
Q9669 abrus preca
Q04072 sambucus ni
Q00980 luffa cylin
Q41358 sambucus ni
Q81KQ5 viscum albu
Q22415 sambucus ni
Q9M654 polygonatum
Q81KQ4 viscum albu
Q81KQ6 viscum albu
Q9F5H2 momordica c
Q9FUV7 momordica c
Q8W243 viscum albu
Q8W243 viscum albu
P91543 sambucus ni
Q81KQ6 viscum albu
Q41257 momordica c
Q81KQ6 viscum albu
Q04358 iris hollan
Q8W2E7 iris hollan
Q04356 iris hollan
Q04356 iris hollan
Q9M653 polygonatum
Q8GZ99 euphorbia s
Q8VYU0 jatrophia cu
Q8W2E8 iris hollan

RESULT 1

Q41174	PRELIMINARY;	PRT;	541 AA.
ID	Q41174		
AC	Q41174;		
DT	01-NOV-1996 (TRENBLrel. 01, Created)		
DT	01-NOV-1996 (TRENBLrel. 01, Last sequence update)		
DE	01-MAR-2003 (TRENBLrel. 23, Last annotation update)		
DE	Protein A chain (EC 3.2.2.22) (rRNA N-glycosidase)		
DE	(Fragment).		
OS	Ricinus communis (Castor bean).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid 1; Malpighiales; Euphorbiaceae; Ricinus.		
OX	NCBI_TaxID=3988;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92338377; PubMed=1633311;		
RA	Roberts L.M., Tregear J.W., Lord J.M.;		
RT	"Molecular cloning of ricin.;"		
RT	Targeted diagn. Ther. 7:81-97(1992).		
CC	!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.		
CC	!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.		
DR	EMBL; S40366; A822382.1; -		
DR	HSSP; P02879; 1BR6.		
DR	InterPro; IPR000772; Ricin_B_lectin.		
DR	InterPro; IPR001574; RIP.		
DR	InterPro; IPR001400; Somatotropin.		
DR	Pfam; PF00652; Ricin_B_lectin; 6.		
DR	Pfam; PF00161; RIP; 1.		
DR	PRINTS; P000396; SHIGARICIN.		
DR	SMART; SM00458; RICIN; 2.		
DR	PROSITE; PS00231; RICIN_B_LECTIN; 2.		
DR	PROSITE; PS00275; SHIGA_RICIN; 1.		
DR	PROSITE; PS00338; SOMATOTROPIN_2; 1.		
DR	HydroLase; Toxin.		
FT	NON TER		
FT	SEQUENCE 541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;		
SQ			


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Query Match      98.8%; Score 1007; DB 10; Length 541;
Best Local Similarity 99.5%; Pred. No. 1.7e-86;
Matches 195; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKOYPIINFAGTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVEL 62
DB 3 PKOYPIINFAGTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVEL 62

QY 63 SNHAELSVTLALDVTNAYVGVYAGNSAYFFHPDQEDAEAIHLFTDQVNRVTFAGGNY 122
DB 63 SNHAELSVTLALDVTNAYVGVYAGNSAYFFHPDQEDAEAIHLFTDQVNRVTFAGGNY 122

QY 123 YDLEOLAGNLRNIELGNGLPEEALISALYYSTGGTQPLTLARSFIIQMISEARFQ 182
DB 123 YDLEOLAGNLRNIELGNGLPEEALISALYYSTGGTQPLTLARSFIIQMISEARFQ 182

QY 183 YIEGEMTRIRYNRS 198
DB 183 YIEGEMTRIRYNRS 198

RESULT 2
Q94BW3 PRELIMINARY; PRT; 580 AA.
AC Q94BW3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin III precursor
DE (EC 3.2.2.22) (tRNA N-glycosidase).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AY039803; AAK82460.1;
CC InterPro; IPR000772; Ricin_B_lectin.
CC InterPro; IPR001574; RIP.
CC Pfam; PF00652; Ricin_B_lectin; 6.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC SMART; SM00458; RICIN; 2.
CC PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN III.
SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7FB558 CRC64;

Query Match      39.4%; Score 401.5; DB 10; Length 580;
Best Local Similarity 50.0%; Pred. No. 2.8e-29;
Matches 94; Conservative 28; Mismatches 59; Indels 7; Gaps 5;

QY 6 YPIINFAGTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVELSN- 64
DB 33 YQTVFTTKNATKTSYQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW 91

QY 65 HAEISVTLALDVTNAYVGVYAGNSAYFFHPDQEDAEAIHLFTDQVNRVTFAGGNYD 124
DB 92 AADSPVTLADVNTNAYVAVYTGSGSFLEARNPD--PAIENLLPDTK-RYTFPFGSGYT 148

QY 125 RLEOLAGNLRNIELGNGLPEEALISALYYSTGGTQPLTLARSFIIQMISEARFQYI 184
DB 149 DLERVAGERREIEILLGMDPLENALSINL--NQQRALARSLLIVVIQMAEAVRFRFI 206

Query Match      39.0%; Score 397.5; DB 10; Length 580;
Best Local Similarity 49.5%; Pred. No. 6.7e-29;
Matches 93; Conservative 30; Mismatches 58; Indels 7; Gaps 5;

QY 6 YPIINFAGTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVELSN- 64
DB 33 YQTVFTTKNATKTSYQFIEALRAQLASGEE-PHGIPVMRDSGTVPDSKRFILVELSNW 91

QY 65 HAEISVTLALDVTNAYVGVYAGNSAYFFHPDQEDAEAIHLFTDQVNRVTFAGGNYD 124
DB 92 AADSPVTLADVNTNAYVAVYTGSGSFLEARNPD--PAIENLLPDTK-RYTFPFGSGYT 148

QY 125 RLEOLAGNLRNIELGNGLPEEALISALYYSTGGTQPLTLARSFIIQMISEARFQYI 184
DB 149 DLERVAGERREIEILLGMDPLENALSINL--WTSNLNQQRALARSLLIVVIQMAEAVRFRFI 206

Query Match      39.0%; Score 397.5; DB 10; Length 580;
Best Local Similarity 49.5%; Pred. No. 6.7e-29;
Matches 93; Conservative 30; Mismatches 58; Indels 7; Gaps 5;

QY 6 YPIINFAGTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVELSN- 64
DB 33 YQTVFTTKNATKTSYQFIEALRAQLASGEE-PHGIPVMRDSGTVPDSKRFILVELSNW 91

QY 65 HAEISVTLALDVTNAYVGVYAGNSAYFFHPDQEDAEAIHLFTDQVNRVTFAGGNYD 124
DB 92 AADSPVTLADVNTNAYVAVYTGSGSFLEARNPD--PAIENLLPDTK-RYTFPFGSGYT 148

QY 125 RLEOLAGNLRNIELGNGLPEEALISALYYSTGGTQPLTLARSFIIQMISEARFQYI 184
DB 149 DLERVAGERREIEILLGMDPLENALSINL--WTSNLNQQRALARSLLIVVIQMAEAVRFRFI 206
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Query Match      98.8%; Score 1007; DB 10; Length 541;
Best Local Similarity 99.5%; Pred. No. 1.7e-86;
Matches 195; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PKOYPIINFAGTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVEL 62
DB 3 PKOYPIINFAGTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVEL 62

QY 63 SNHAELSVTLALDVTNAYVGVYAGNSAYFFHPDQEDAEAIHLFTDQVNRVTFAGGNY 122
DB 63 SNHAELSVTLALDVTNAYVGVYAGNSAYFFHPDQEDAEAIHLFTDQVNRVTFAGGNY 122

QY 123 YDLEOLAGNLRNIELGNGLPEEALISALYYSTGGTQPLTLARSFIIQMISEARFQ 182
DB 123 YDLEOLAGNLRNIELGNGLPEEALISALYYSTGGTQPLTLARSFIIQMISEARFQ 182

QY 183 YIEGEMTRIRYNRS 198
DB 183 YIEGEMTRIRYNRS 198

RESULT 2
Q94BW3 PRELIMINARY; PRT; 580 AA.
AC Q94BW3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin III precursor
DE (EC 3.2.2.22) (tRNA N-glycosidase).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AY039803; AAK82460.1;
CC InterPro; IPR000772; Ricin_B_lectin.
CC InterPro; IPR001574; RIP.
CC Pfam; PF00652; Ricin_B_lectin; 6.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC SMART; SM00458; RICIN; 2.
CC PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN III.
SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7FB558 CRC64;

Query Match      39.4%; Score 401.5; DB 10; Length 580;
Best Local Similarity 50.0%; Pred. No. 2.8e-29;
Matches 94; Conservative 28; Mismatches 59; Indels 7; Gaps 5;

QY 6 YPIINFAGTAGATVQSYNFIKAVRGLTTGADVRHEIPVLPNVRGLPINQRFILVELSN- 64
DB 33 YQTVFTTKNATKTSYQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW 91

QY 65 HAEISVTLALDVTNAYVGVYAGNSAYFFHPDQEDAEAIHLFTDQVNRVTFAGGNYD 124
DB 92 AADSPVTLADVNTNAYVAVYTGSGSFLEARNPD--PAIENLLPDTK-RYTFPFGSGYT 148

QY 125 RLEOLAGNLRNIELGNGLPEEALISALYYSTGGTQPLTLARSFIIQMISEARFQYI 184
DB 149 DLERVAGERREIEILLGMDPLENALSINL--NQQRALARSLLIVVIQMAEAVRFRFI 206
```

OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN SEQUENCE FROM N.A.
RP Cinnamomum camphora (Camphor tree).
RA Xie L., Liu W.-Y., Wang E.-D.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AY039801; AAK82458.1; -.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR PRINTS; PR00161; RIP; 1.
DR SMART; SM00458; SHIGARICIN.
DR PROSITE; PS00396; SHIGARICIN.
DR PROSITE; PS00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 581
FT POTENTIAL.
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN I.
SQ SEQUENCE 581 AA; 64215 MW; 658F5F8F8A3D196 CRC64;
Query Match 39.0%; Score 397.5; DB 10; Length 581;
Best Local Similarity 50.0%; Pred. No. 6.7e-29;
Matches 94; Conservative 27; Mismatches 60; Indels 7; Gaps 5;
QY 6 YPIINFATTAGATVQSYTFIRAVRGRLTGTADVRHEIPVLPNRVGLPINQRFILVLSN- 64
DB 33 YQTVFTTKATKTSYQFIEALRAQLASGEE-PHGIPVWRERSTVPDSKRFILVLSNW 91
QY 65 HAELSVTLALDVTNAYVVGVRAGNSAYFFHFDNODAEAIHTLFTDQNRVTEAFGGNYD 124
DB 92 AADSPVTLAVDTNAYVAVRGSGSFLEDRNPD--PAIENLLPDTK-RYTFPFGSGYT 148
QY 125 RLEQLAGMLRENIENGNGPLEAIALYVYTGSTQPLTARSFICICMISEAARFOYI 184
DB 149 DLEGVAGERREILLGMDPLENAISALWISNL--NQQRALARSLLVVIQWVAEVRFRFI 206
QY 185 EGEWRTI 192
DB 207 EYRVGSI 214
RESULT 5
Q9FV22
ID Q9FV22 PRELIMINARY; PRT; 549 AA.
AC Q9FV22;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (rRNA
DE N-glycosidase) (fragment).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN SEQUENCE FROM N.A.
RP Cinnamomum camphora (Camphor tree).
RA Xie L., Liu W.-Y., Wang E.-D.;
RT "Molecular cloning of cinnamomin A-, B-chain and the expression,
RT purification, characterization and mutagenesis of the A-chain";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF259548; AAF68978.2; -.
DR HSSP; P02879; 2AAL.

DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; SHIGARICIN.
DR PROSITE; PS00396; SHIGARICIN.
DR PROSITE; PS00458; RICIN; 2.
KW Hydrolase; Toxin.
FT NON_TER 1
FT SIGNAL 1 25
SQ SEQUENCE 549 AA; 60648 MW; 02607FE607CA44B0 CRC64;
Query Match 38.8%; Score 395.5; DB 10; Length 549;
Best Local Similarity 50.0%; Pred. No. 9.6e-29;
Matches 94; Conservative 27; Mismatches 60; Indels 7; Gaps 5;
QY 6 YPIINFATTAGATVQSYTFIRAVRGRLTGTADVRHEIPVLPNRVGLPINQRFILVLSN- 64
DB 1 YQTVFTTKATKTSYQFIEALRAQLASGEE-PHGIPVWRERSTVPDSKRFILVLSNW 59
QY 65 HAELSVTLALDVTNAYVVGVRAGNSAYFFHFDNODAEAIHTLFTDQNRVTEAFGGNYD 124
DB 60 AADSPVTLAVDTNAYVAVRGSGSFLEDRNPD--PAIENLLPDTK-RYTFPFGSGYT 116
QY 125 RLEQLAGMLRENIENGNGPLEAIALYVYTGSTQPLTARSFICICMISEAARFOYI 184
DB 117 DLEGVAGERREILLGMDPLENAISALWISNL--NQQRALARSLLVVIQWVAEVRFRFI 174
QY 185 EGEWRTI 192
DB 175 EYRVGSI 182
RESULT 6
Q04367
ID Q04367 PRELIMINARY; PRT; 563 AA.
AC Q04367;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA
DE N-glycosidase).
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN SEQUENCE FROM N.A.
RX MEDLINE=98112023; PubMed=9450339;
RA Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
RA Peumans W.J.;
RT "The major elderberry (Sambucus nigra) fruit protein is a lectin
RT derived from a truncated type 2 ribosome-inactivating protein.";
RL Plant J. 12:1251-1260(1997).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; U76524; AAC15886.1; -.
DR HSSP; P02879; 2AAL.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA RICIN; 1.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 297
FT POTENTIAL.
FT RIBOSOME INACTIVATING PROTEIN, A CHAIN.
FT RIBOSOME INACTIVATING PROTEIN, B CHAIN.
SQ SEQUENCE 563 AA; 62336 MW; 3ED2B6C08E796205 CRC64;

Query Match	34.4%	Score 350.5;	DB 10;	Length 563;
Best Local Similarity	41.6%;	Pred. No. 1.8e-24;		
Matches 79;	Conservative 40;	Mismatches 56;	Indels 15;	Gaps 4;

6 YPIINFTTAGATVQSYTNFIRAVRGLTTCADVREHIEPVLNVRGLPINQRFLIVELSNH 65
||:||| ||| :||: :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
28 YPSVSFNLAGAKSATYRFELKNIPTIVATGYEVNGLPVLRRESEVOVKRRFVLVLNNY 87

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66 AELSVTLALDVTNAYVVVGYRAGNSAYFFHPDNQDEAEI--THLFTDVQNRYTFAFEGNY 123
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
09 VGVSTYMTAIGTUMVIATVIAIDGIANQVDFVWATQYAGNTIVWGFQCHMTDEMGNY 141
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124 DRLEQIAGNLRNENIELGNGLPLEEIALSALYYYSTGGTQLPPTARSFFICQMISEAARQY 183

184 IEGERTRIR 193

193 1E9EVARSJQ 204

2011 E 7

Q9AVR2 PRELIMINARY; PRT; 564 AA.

T 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
T 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
E Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA

EBU1.
Sambucus ebulus.
Eukaryota: Viridiplantae: Streptophyta: Tracheophyta:

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
NCBI TaxID=28503;
[4]

P P SEQUENCE FROM N.A.
C TISSUE=Leaf;
A Girbes T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;

Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 EMBL: AJ400822; CAC33178.1; -.
 HSP; P02879; 2AA1.
 InterPro: IPR000372. Picin p lectin

R InterPro; IPR001574; RIP.
R Pfam; PF00652; Ricin_B_lectin; 6.
R Pfam; PF00161; RIP; 1.

R SMART; SM00458; RICIN; 2.
R PROSITE; PS50231; RICIN_B_LECTIN; 2.
R PROSITE; PS00275; SHIGA_RICIN; 1.

	SIGNAL	1	25	POTENTIAL.
T	CHAIN	26	298	EBULIN L A-CHAIN.
T	CHAIN	299	554	EBULIN I B-CHAIN

Q SEQUENCE 564 AA; 62694 MW; 8261681A6DB55CB8 CRC64;
Query Match 34.1%; Score 347.5; DB 10; Length 564;

Matches 78; Conservative 41; Mismatches 56; Indels 15; Gaps 5

28 YPSYSENLAKASTYYRDFLNLRDRVATGTYEVNGLPVLRRESEVQVKNRFVLRITLY 87

b 88 NGDTWTSADVDTNLYLVAFSANGNSYFF-----KDATELQKSNFLGTTQHTLSPTGNY 141

QY	124	DRLEQLAGNLRNLEIENGNGPLBEALYYSTGGTQLPTIARSFTICIMISEAARFQY	183
Db	142	DNLETAAGTRRESIEIIGPNLPDGAITSLWY--DGG-----VARSLLIOMVPEAARFY	194

QY	184	IEGENRTRIR	193
		: ::	
Db	195	IEQEVRRSLQ	204

RESULT 8
005076

ID Q06076 PRELIMINARY; PRT; 528 AA.
AC Q06076;
DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Abrin-d (BC 3.2.2.2) (rRNA N-glycosidase) (Fragment).
 QS Abrus precatorius (indian licorice) (Crab's eye).
 OS

[illegible]

RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=93132798; PubMed=8421313;

RT "Primary structure of three distinct isoabirins determined by cDNA
RT sequencing: conservation and significance.";
RT J. Mol. Biol. 229:263-267(1993).
RL

CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: M983346; AAA32626.1; -.

DK HSSP; F11140; IABK.
DR InterPro; IPR000772; Ricin B lectin.
DR InterPro; IPR01574; RIP.
DR pfam; PF00553; Ricin B lectin. 6

DR pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.

DR	PROSITE; PS00275; SHIGA_RICIN; 1.
FT	Hydrolase; Toxin.
KW	NON TER 1

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FI NON-LEK 328
SQ SEQUENCE 528 AA: 58870 MW: 62ED42FB8FFE60F8 CRC64;
Query Match 33 8%: SCORE 144.5: DB 10: Length 528:

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Best Local Similarity 45.0%; Pred. No. 5.9e-24;
Matches 85; Conservative 24; Mismatches 71; Indels 9; Gaps 4

Db 1 QDQVIKETTEGATSSQYKQFIEALRQRLTGG--LIHDIPVLDPPTTVEERNRYITVELSN 58

59 SERESIEVGIDVTNAYVYAYRAGSQSYFL---RDAPASASTYLPFGTQ-RYSLRFDGSGY 114

Qy	125 RUEQAGNLRNIELGNGPLESAISALUYYSYTGTLPLARSPFLCICIMISEAAAFQJ	187
Qy	125 RUEQAGNLRNIELGNGPLESAISALUYYSYTGTLPLARSPFLCICIMISEAAAFQJ	187
Db	115 DIERWAHQTREESLGLQALTHAIS--FLRSGASNDEEKARTLJVIIQMASEAARYRCI	171

Qy	185	E	G	E	M	R	T	R	193
			:						
Db	172	S	N	R	V	G	V	S	180

RESULT 9
C94KE4

ID	C94KE4;	PRELIMINARY;	PRT;	289 AA.
AC	C94KE4;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		

01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase).
GN TCS.
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
ON NCBI_TaxID=3677;
RX [1]
RY SEQUENCE FROM N.A.
RA Yuan H., Wang L., Wang Y., An C., Chen Z.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF367252; AAK52960.1; -;
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA-RICIN; 1.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 23
FT CHAIN 24 270
FT TRICHOSANTHIN.
SQ SEQUENCE 289 AA; 31706 MW; A6D5602549CA5657 CRC64;
Query Match 33.4%; Score 340; DB 10; Length 289;
Best Local Similarity 39.5%; Pred. No. 6.8e-24;
Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps 5
QY 9 INFTTAGATVQSYNTFNRAVGRLLTGTADVRRHEIPVLPENRVGLPINFQRFILVELSNHAEL 68
Db 25 VSPRLSGATSSSYGVFIENLRKALPNERKL-YDIPLL--RSSLPQSQRVALIHLTNYADE 81
QY 69 SVTLALDVTHAYVYGYRAGNSAYFEHPDNQDEA-EAITHLFTDVQNRVYTFAGGNYDRLE 127
Db 82 TISVAIDVTNVIYMGYTAGDTSYFF--NEASATEAAKYVFKDSMRKKTILPYSGNYERLQ 138
QY 128 QLQALRENLEIQLNGPLEEALISALYVYTGCTQLPTLARSPFICITQMISEAARFOYIERGE 187
Db 139 TAAGKIRENIPGLPALDSATITLFIYNAN----SASALMWLIQSTSEAAKYKFIEQQ 193
QY 188 MRTRI 192
Db 194 IGKEV 198
RESULT 10
Q9LRE3
ID Q9LRE3 PRELIMINARY; PRT; 247 AA.
AC Q9LRE3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
GN TBK.
OS Trichosanthes sp. Bac Kan 8-98.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
ON NCBI_TaxID=118182;
RX [1]
RY SEQUENCE FROM N.A.
RA Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
RL "Genomic DNA clone for mature typ-1 ribosome-inactivating protein from
RL Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNHS (Hanoi).";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AB039324; BAA92530.1; -;
DR HSSP; P09989; 1MRJ.
DR InterPro; IPR001574; RIP.

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DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Toxin.
FT NON_TER 1
FT NON_TER 247
SQ SEQUENCE 247 AA; 27199 MW; 89811AC32892F03F CRC64;

Query Match
Best Local Similarity 33.2%; Score 338; DB 10; Length 247;
Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;

QY 9 INFTTAGATVQSYNTFIRAVRGLTTCADVRHEIPVLPNVRVGLPINORFILVELSNHAEL 68
Db 2 VSPFLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSTLPGSQRYALVHLTNYADE 58
QY 69 SVTLALDVTNAYVVGVRAGNSAYFFHPDNCEDA-EAITHLFTDVQNYRTFAFGNYDRLE 127
Db 59 TISVAIDVTNVYMGVRAGDTSYFF--NEASATEAKYVFKDAKRVTLFPGSYNERLQ 115
QY 128 QLAGNIRENIEELGNPLEEASIALSYVSTGTOPLTLARSFIICIMISPAARFOYIEGE 187
Db 116 IAAKGIRENIEPLGLPALDSAITTLFYNNAN---SAASALMVLIOQSTSEAAARYKFFIEQ 170
QY 188 MRTRI 192
Db 171 IGKRV 175

RESULT 11
Q41216 PRELIMINARY; PRT; 289 AA.
ID Q41216
AC Q41216;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase).
GN TRICHOSANTHIN, TCS.
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosoids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OC NCBI_TaxID=3677;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94271613; PubMed=8003348;
RT Zheng H., Wang B., Shaw P., Yeung H.;
RT "[Cloning and DNA sequencing of the gene encoding trichosanthin].";
RL I Chuan Hsueh pao 21:42-51(1994).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; S70176; RAB31048.1; -.
DR HSPSP; P09989; IMRJ.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Toxin.
SQ SEQUENCE 289 AA; 31650 MW; 286AC14D48BCAL75 CRC64;

Query Match
Best Local Similarity 33.2%; Score 338; DB 10; Length 289;
Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps 5;

QY 9 INFTTAGATVQSYNTFIRAVRGLTTCADVRHEIPVLPNVRVGLPINORFILVELSNHAEL 68
Db 25 VSPFLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALVHLTNYADE 81
QY 69 SVTLALDVTNAYVVGVRAGNSAYFFHPDNCEDA-EAITHLFTDVQNYRTFAFGNYDRLE 127
Db 82 TISVAIDVTNVYMGVRAGDTSYFF--NEASATEAKYVFKDAKRVTLFPGSYNERLQ 138

```

QY 128 QLAGNLRNIELNGPLEEALSAIYVYSGTGTPLTARSFICIMISEAARFQIEG 187
 DB 139 TAAGKIRENIPGLPALDSAITFLFYNNAN-----SAAALMWLIQSTSEAAKYKEIOQ 193
 QY 188 MRTRI 192
 DB 194 IGRV 198

RESULT 12
 Q38760
 ID Q38760 PRELIMINARY; PRT; 252 AA.
 AC Q38760;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Abrin-E (RRNA N-glycosidase) (EC 3.2.2.22) (fragment).
 GN RIP.
 OS Abrus precatorius (Indian licorice) (Crab's eye).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
 OC NCBI_TaxID=3816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RX MEDLINE=91201329; PubMed=2016300;
 RA Evensen G., Mathiesen A., Sundan A.;
 RT "Direct molecular cloning and expression of two distinct abrin A-
 RT chains.";
 RL J. Biol. Chem. 266:6848-6852 (1991).
 CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
 CC ABRIN-A IS MORE TOXIC THAN RICIN.
 CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
 CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
 CC PRECEDES ENDOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
 CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
 CC PROTEINS. BELONGS TO TYPE 2 RIP.
 DR EMBL; X54872; CAA38654.1; -;
 DR HSP; P11140; IABR.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA RICIN; 1.
 KW Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
 FT CHAIN 1 252 ABRIN E, A CHAIN (BY SIMILARITY).
 FT NON TER 252
 SQ SEQUENCE 252 AA; 28309 MW; BBFC846B9E92B5DE CRC64;

Query Match 33.0%; Score 336.5; DB 10; Length 252;
 Best Local Similarity 44.9%; Pred. No. 1.2e-23;
 Matches 83; Conservative 24; Mismatches 69; Indels 9; Gaps 4;

QY 9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNVRGLPQINQRFILVELSNHAE 68
 DB 6 IKFSTEGATSQYKQFIEALRERLGG--LIHIDPVLDRPTVEERNYITVELSNGERE 63
 QY 69 SVTLALDVNAYVYVGRAGNSAYFFHPDQDEAEAI--THLFTDVQNRVYTFAGGNYDRLEQ 128
 DB 64 SIEVGIDVTNAYVAYRAGSQSYFL---RDAPASASTYLTGTQ-RVSLRFDGSGYGLER 119
 QY 129 LAGNLRNIELNGPLEEALSAIYVYSGTGTPLTARSFICIMISEAARFQIEGEM 188
 DB 120 WAHQTRQISLGLQALTHAIS---FLRSGASNDEKATLVIQMASEAARYIISNRV 176
 QY 189 RTRIR 193

DB 177 GVSIR 181

RESULT 13
 Q945S2
 ID Q945S2 PRELIMINARY; PRT; 563 AA.
 AC Q945S2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Ribosome-inactivating protein (EC 3.2.2.22) (rRNA
 DE N-glycosidase).
 GN AVL.
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OC NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Van Damme E.J.M.;
 RT "Characterization and cloning of lectins and ribosome-inactivating
 RT proteins from Sambucus nigra leaves.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC EMBL; AF409135; AAL04123.1; -;
 DR InterPro; IPR001574; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR PRINTS; PR00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS00231; RICIN B LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Toxin.
 SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;

Query Match 32.4%; Score 330.5; DB 10; Length 563;
 Best Local Similarity 39.5%; Pred. No. 1.4e-22;
 Matches 75; Conservative 39; Mismatches 61; Indels 15; Gaps 4;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNVRGLPQINQRFILVELSNH 65
 DB 28 YPSVSNLDGAKSATYRDFLSNLRKTVATGTVEVGLPVLRRSEVQVKSFRFVLPLTNY 87
 QY 66 AELSVTILALDVNAYVYVGRAGNSAYFFHPDQDEAEAI--THLFTDVQNRVYTFAGGNY 123
 DB 88 NGNTVTLAVDVNLYVYVAFSGNANSYFF-----KDATEVQKSNLFVGTQKN-TLSFTGNY 141
 QY 124 DRLEQLAGNLRNIELNGPLEEALSAIYVYSGTGTPLTARSFICIMISEAARFQY 183
 DB 142 DNLETAANTARRESIELGSPSLDGAITSYHGD-----SVARSLLVVIQWSEAAFRY 194
 QY 184 IEGEMRTRIR 193
 DB 195 IEQEVRRSLQ 204

RESULT 14
 Q8GT32
 ID Q8GT32 PRELIMINARY; PRT; 563 AA.
 AC Q8GT32;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein nigrin I precursor
 DE (EC 3.2.2.22).
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:20 ; Search time 32.0534 Seconds
(without alignments)
930.966 Million cell updates/sec

Title: US-10-083-336A-8

Perfect score: 965

Sequence: 1 MVRQYPIINTAGATVQS.....ARFQYIEGEMTRIRYNERS 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_15Jun03.*

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	950	98.4	267	13	AA1980
2	950	98.4	267	21	AA19265
3	941	97.5	267	14	AA19290
4	941	97.5	267	16	AA19302
5	941	97.5	290	18	AA1925136
6	941	97.5	290	18	AA1925136
7	941	97.5	332	8	AA190097
8	941	97.5	332	8	AA190097
9	941	97.5	332	10	AA195639

10	941	97.5	554	16	AA190827
11	941	97.5	562	10	AA190079
12	941	97.5	565	6	AA190166
13	941	97.5	565	22	AA1978300
14	941	97.5	565	22	AA1978304
15	941	97.5	576	8	AA1970326
16	941	97.5	576	18	AA1925787
17	941	97.5	576	20	AA1955892
18	941	97.5	576	21	AA1978592
19	941	97.5	576	22	AA1978301
20	941	97.5	576	22	AA1978302
21	937	97.1	200	9	AA1980164
22	936	97.0	565	7	AA1960240
23	934	96.8	268	14	AA1939570
24	934	96.8	574	8	AA1970325
25	932	96.6	574	10	AA194793
26	931	96.5	534	14	AA1939571
27	930	96.4	332	11	AA1906554
28	927	96.1	267	14	AA1932430
29	924	95.8	267	16	AA1974176
30	851.5	88.2	540	18	AA1925143
31	851.5	88.2	540	18	AA1925140
32	791.5	82.0	534	8	AA1970324
33	718	74.4	280	10	AA1956648
34	336	34.8	247	16	AA1967359
35	336	34.8	247	21	AA1969048
36	336	34.8	248	11	AA1907518
37	336	34.8	248	13	AA1925573
38	336	34.8	267	18	AA1925140
39	336	34.8	267	18	AA1925140
40	336	34.8	289	11	AA197514
41	336	34.8	289	13	AA1925572
42	336	34.8	289	13	AA1929272
43	336	34.8	289	13	AA1929272
44	336	34.8	289	15	AA1929286
45	336	34.8	289	15	AA1929286

ALIGNMENTS

RESULT 1

AA190722
ID AA190722 standard; Protein; 267 AA.
XX
AC AA190722;
XX
DT 25-MAR-2003 (updated)
DT 08-FEB-1993 (first entry)
XX
DE Ricin A from pIC1102.
XX
KW pH; temperature; cultivation; host; soluble.
OS Synthetic.
PN EP501692-A2.
XX
PD 02-SEP-1992.
XX
PF 21-FEB-1992; 92EP-0301466.
XX
PR 26-FEB-1991; 91GB-0003925.
PR 26-FEB-1991; 91GB-0003926.
PR 26-FEB-1991; 91GB-0004016.
(ICIL) IMPERIAL CHEM IND PLC.
(ZENE) ZENECA LTD.
PI Pitton JE, Hockney RC, Kara BV;
XX WPI; 1992-294124/36.
DR N-PSDB; AAQ27876.

XX
PT

Prepn. of soluble recombinant polypeptide(s), esp. ricin A - by adjusting pH and/or temp. during cultivation to increase yield of soluble prod.

XX
PT

Disclosure; Fig 9; 49pp; English.

XX
PS

Prepn. of ricin A comprises cultivating a host, including a DNA sequence which encodes ricin A, e.g. from pIC1102, in a nutrient medium for an initial period at a first pH value which favours growth of the host; and cultivation the host for a further period at a pH lower than the first pH value, and opt. cooling the host during the terminal portion of the cultivation and harvesting the host during the terminal portion. By adjusting the pH and temp. during the cultivation of hosts, high yields of soluble recombinant ricin A are obtained.

XX
CC

(Updated on 25-MAR-2003 to correct PN field.)

XX
CC

(Updated on 25-MAR-2003 to correct PA field.)

XX
SQ

Sequence 267 AA;

Query Match

Best Local Similarity 98.4%; Score 950; DB 13; Length 267;

Matches 188;

Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY

1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILV 50

Db

1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNRVGLPINQRFILV 60

QY

51 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 110

Db

61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120

QY

111 GNYDRLEQLAGNLRNIELGNGPLEEASALYYSTGTGTLPTLARSFIIICQMISEAAR 170

Db

121 GNYDRLEQLAGNLRNIELGNGPLEEASALYYSTGTGTLPTLARSFIIICQMISEAAR 180

QY

171 FOYIEGEMRTRIRYNRRS 198

Db

181 FOYIEGEMRTRIRYNRRS 198

RESULT 2

AAB19265

ID AAB19265 standard; protein; 267 AA.

XX
AC

AAB19265;

XX
AC

19-FEB-2001 (first entry)

XX
DT

Amino acid sequence of a human ricin toxin A chain (RTA).

XX
DE

Immunotoxin; cytokine; vascular leak syndrome; VLS; lymphoma; myeloma; graft versus host disease; metastatic lesion tumour; tumour; immunotoxin; ricin toxin A chain.

XX
KWXX
KWXX
KWXX
OSXX
OSXX
FHXX
FHXX
FTXX
FTXX
FNXX
XXXX
PDXX
XXXX
PFXX
PRXX
XXXX
PAXX
XXXX
PI

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DR

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WPI; 2000-664922/64.

Modifying the ability of a proteinaceous composition to induce a toxic effect for reducing vascular leak syndrome, comprises identifying at least one specified amino acid sequence and altering it -

Example 1; Page 119-120; 125pp; English.

The specification describes a method for producing immunotoxins and cytokines with a reduced ability to promote vascular leak syndrome (VLS). The immunotoxins are useful for treating graft versus host disease, non-Hodgkin's and Hodgkin's lymphoma, myeloma, metastatic lesion tumours and some type of solid tumours. The present sequence represents an immunotoxin (ricin toxin A chain) which induces VLS. The VLS-inducing motif can be mutated or deleted so that VLS is not induced.

Sequence 267 AA;

Query Match 98.4%; Score 950; DB 21; Length 267;

Best Local Similarity 94.9%; Pred. No. 1.1e-93;

Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY

1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILV 50

Db

1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNRVGLPINQRFILV 60

QY

51 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 110

Db

61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120

QY

111 GNYDRLEQLAGNLRNIELGNGPLEEASALYYSTGTGTLPTLARSFIIICQMISEAAR 170

Db

121 GNYDRLEQLAGNLRNIELGNGPLEEASALYYSTGTGTLPTLARSFIIICQMISEAAR 180

QY

171 FOYIEGEMRTRIRYNRRS 188

Db

181 FOYIEGEMRTRIRYNRRS 198

RESULT 3

AAR37290

ID AAR37290 standard; protein; 267 AA.

XX
AC

AAR37290;

XX
ACXX
DTXX
DTXX
DTXX
DTXX
DEXX
XXXX
KWXX
KWXX
OSXX
OSXX
PNXX
XXXX
XXXX
PDXX
XXXX
PFXX
XXXX
PRXX
PRXX
XXXX
PAXX
XXXX
FIXX
XXXX
DRXX
XX

Type II ribosome-inactivating protein; type II RIP; gelonin; momordin; immunconjugate; autoimmune disease; cell killing; toxin.

Unidentified.

WO9309130-A1.

13-MAY-1993.

04-NOV-1992; 92WO-US09487.

04-NOV-1991; 91US-0787567.

19-JUN-1992; 92US-0901707.

(XOMA) XOMA CORP.

Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

WPI; 1993-167617/20.

PT Analogues of type I ribosome inactivating protein - useful as
 PT cytotoxic agents, immuno toxins for treating autoimmune diseases,
 PT cancer, graft versus host disease and selective cell killing in-vivo
 XX
 PS Claim 1; Page 92; 163pp; English.

XX The invention covers analogues of Type I RIPs. Ricin is a Type II
 CC RIP whose A chain is homologous to plant type I RIPs. The analogues
 CC of the invention have a cysteine available for intermolecular
 CC disulphide bonding at an amino acid position corresp. to a position
 CC not naturally available for bonding; the cys residue is located in
 CC the C-terminal region of the analogue between a position corresp. to
 CC amino acid 251 and the C-terminus of ricin A chain. The analogues are
 CC pref. joined via a disulphide linkage to a molecule which specifically
 CC binds to a target cell, e.g. an antibody fragment.
 CC (Updated on 09-JAN-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 267 AA;

Query Match 97.5%; Score 941; DB 14; Length 267;
 Best Local Similarity 94.9%; Pred. No. 1e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFITAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 3 PKQYPIINFITAGATVQSYTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINQRFILVEL 62
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 112
 DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 122
 QY 113 YDRLEQLAGNLRENIELGNGLPLEAISALYYVSTGGTQLPTLARSFFIICQMISEAARFQ 172
 DB 123 YDRLEQLAGNLRENIELGNGLPLEAISALYYVSTGGTQLPTLARSFFIICQMISEAARFQ 182
 QY 173 YIEGEMTRIRYNRRS 188
 DB 183 YIEGEMTRIRYNRRS 198

RESULT 4
 AAR63902
 ID AAR63902 standard; protein; 267 AA.
 XX AC AAR63902;

DT 25-MAR-2003 (updated)
 DT 27-JUL-1995 (first entry)

DE Ricin A-chain (RTA).

KW Ricin A chain; RTA; ribosome-inactivating proteins; RIPs;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.

XX Ricinus communis.

XX WO9426910-A1.

XX 24-NOV-1994.

PF 12-MAY-1994; 94WO-US05348.

PR 12-MAY-1993; 93US-0064691.

PA (XOMA) XOMA CORP.

XX Better MD, Carroll SS, Studnicka GM, Carroll SF;

XX WPI; 1995-006804/01.

XX Polynucleotide(s) encoding type I ribosome-inactivating proteins

PT - which are suitable for use as components of cytotoxic
 PT therapeutic agents.

XX Example 3; Fig 1; 221pp; English.

XX AAR63902 is the ricin A chain gene product, it is analogous to the
 CC ribosome-inactivating proteins (RIPs) described in AAR63903-R63911.
 CC RIPs are the key components of cytotoxic therapeutic agents (CTAs),
 CC which include gene fusion products and immunoconjugates. CTAs may
 CC be used to selectively eliminate any cell type to which a RIP
 CC component is targeted, by the specific binding capacity of the
 CC second component of the agent. They can be used in the treatment
 CC of diseases where the elimination of a particular cell type is
 CC desired, such as autoimmune disease, cancer and graft-versus-host
 CC disease.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 267 AA;

Query Match 97.5%; Score 941; DB 16; Length 267;
 Best Local Similarity 94.9%; Pred. No. 1e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFITAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 3 PKQYPIINFITAGATVQSYTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINQRFILVEL 62
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 112
 DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 122
 QY 113 YDRLEQLAGNLRENIELGNGLPLEAISALYYVSTGGTQLPTLARSFFIICQMISEAARFQ 172
 DB 123 YDRLEQLAGNLRENIELGNGLPLEAISALYYVSTGGTQLPTLARSFFIICQMISEAARFQ 182
 QY 173 YIEGEMTRIRYNRRS 188
 DB 183 YIEGEMTRIRYNRRS 198

RESULT 5
 AAW25136
 ID AAW25136 standard; protein; 290 AA.

XX AC AAW25136;

DT 25-MAR-2003 (updated)

DT 02-DEC-1997 (first entry)

DE Ricin A-chain ribosome inhibitory protein inactive precursor.

KW Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; Barley translation inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A chain; Saporin; SUT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome.

OS Synthetic.

XX US5646026-A.

XX 08-JUL-1997.

XX 07-JUN-1995; 95US-0485286.

XX 09-DEC-1992; 92US-0987927.

XX 11-JUN-1990; 90US-0535636.

XX 26-JAN-1995; 95US-0378761.

XX 07-JUN-1995; 95US-0485286.

XX (DOWC) DOWELANCO.

XX PI Hey TD, Morgan AER, Walsh TA;
 XX DR WPI; 1997-362934/33.
 XX PT DNA encoding pro-ribosome inactivating proteins - inactive
 XX PT precursors of ribosome inactivating proteins; can be expressed in
 XX PT eukaryotic cells without causing cell death
 XX PS
 XX PS Claim 4; Column 91-94; 186pp; English.
 XX CC AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
 XX CC which was engineered to contain a selectively removable internal peptide
 XX CC linker sequence separating the alpha and beta units of the RIP. When
 XX CC separated the two units regain activity and are capable of inactivating
 XX CC eukaryotic ribosomes and hence preventing protein production. Many
 XX CC different RIPs may be produced with an internal linker including
 XX CC maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
 XX CC Saporin. The RIPs can be used in the construction of therapeutic
 XX CC toxins targeted to specific cells such as tumour cells via the
 XX CC attachment of a targeting polypeptide, e.g. a monoclonal antibody.
 XX CC A further use is in HIV therapy (see US4869903). There is interest
 XX CC in expressing RIP recombinantly in host eukaryotic cells, because of
 XX CC the capacity to provide post-translational processing. However,
 XX CC RIPs effectively inhibit protein synthesis in eukaryotic cells resulting
 XX CC in cell death. Since the inactive RIP proteins are not cytotoxic to
 XX CC eukaryotic cells, they can be recombinantly expressed in such cells and
 XX CC then converted to active RIP proteins.
 XX CC (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 290 AA;
 Query Match 97.5%; Score 941; DB 18; Length 290;
 Best Local Similarity 94.9%; Pred. No. 1.1e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFATTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 52
 Db 27 PKQYPIINFATTAGATVQSYTNFIRAVRGLTTCGADVREHIEPVLNVRVGLPINQRFILVEL 86
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVNRVYFAFGN 112
 Db 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVNRVYFAFGN 146
 QY 113 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQLPTLARSFTICQIMISEAARFQ 172
 Db 147 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQLPTLARSFTICQIMISEAARFQ 206
 QY 173 YIEGEMTRIRYNRRS 188
 Db 207 YIEGEMTRIRYNRRS 222
 RESULT 6
 AAW21699
 ID AAW21699 standard; Protein; 290 AA.
 AC
 XX AAW21699;
 XX 25-MAR-2003 (updated)
 DT 26-SEP-1997 (first entry)
 XX Ricin A-chain RIP.
 XX pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
 XX Ricinus communis.
 OS
 XX Key Location/Qualifiers
 FH Region 152..162
 FT

FT FT /note= "Position of possible insertion of internal
 XX XX peptide linker sequence"
 PN US5635384-A.
 XX 03-JUN-1997.
 PD 26-JAN-1995; 95US-0378761.
 XX 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 XX (DOWC) DOWELANCO.
 PA Hey TD, Morgan AER, Walsh TA;
 XX WPI; 1997-309831/28.
 XX Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 PT internal linker sequences
 XX Claim 2; Column 91-94; 121pp; English.
 XX The sequences given in AAW21698-710 represent Ribosome Inactivating
 CC Proteins (RIP's), which may be used in the construction of the
 CC proRIP of the invention. The proRIP has a selectively removable,
 CC internal peptide linker. The precursor sequence is incapable of
 CC inactivating eukaryotic ribosomes, but can be converted by removal
 CC of the linker into a protein having alpha and beta fragments and being
 CC capable of inactivating eukaryotic ribosomes. RIPs are potent
 CC inhibitors of eukaryotic protein synthesis. They possess a highly
 CC specific N-glycosidase activity which cleaves the glycosidic bond of
 CC adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit
 CC cellular proliferation of cells, e.g. cancer cells and HIV-infected T
 CC cells. The inactive proRIP proteins make it possible to provide protein
 CC synthesis inhibitors with uses in practical and improved ways not before
 CC possible. The RIP can be used to make cytotoxic conjugates.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 290 AA;
 Query Match 97.5%; Score 941; DB 18; Length 290;
 Best Local Similarity 94.9%; Pred. No. 1.1e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFATTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 52
 Db 27 PKQYPIINFATTAGATVQSYTNFIRAVRGLTTCGADVREHIEPVLNVRVGLPINQRFILVEL 86
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVNRVYFAFGN 112
 Db 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDQVNRVYFAFGN 146
 QY 113 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQLPTLARSFTICQIMISEAARFQ 172
 Db 147 YDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQLPTLARSFTICQIMISEAARFQ 206
 QY 173 YIEGEMTRIRYNRRS 188
 Db 207 YIEGEMTRIRYNRRS 222
 RESULT 7
 AAP70037
 ID AAP70037 standard; protein; 332 AA.
 XX AAP70037;
 XX 09-APR-1991 (first entry)
 DT Ricin A.
 DE

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XX Ricin A; Met-aminopeptidase.
KW Escherichia coli.
XX EP129237-A.
XX PD 22-APR-1987.
XX PF 19-SEP-1986; 86EP-0307242.
XX PR 06-MAY-1986; 86US-0860330.
XX FR 20-SEP-1985; 85US-0778414.
XX PA (CETU ) CETUS CORP.
XX PI Benbassat A, Bauer KA, Chang S, Chang SY;
XX WPI; 1987-110172/16.
XX DR N-PSDB; AAN70152.
XX PT N-terminal methionine free proteins prodn. - by using host
XX transformed with vector to express a methionine-amino-peptidase
XX PS Disclosure; Fig. 4; 20pp; English.
XX CC Ricin A may be produced in a form which lacks an N-terminal Met
XX using Met-aminopeptidase from E.coli.
XX SQ Sequence 332 AA;
    Query Match 97.5%; Score 941; DB 8; Length 332;
    Best Local Similarity 94.9%; Pred. No. 1.4e-92;
    Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFTTAGATVQSNTNFIRAVRGRLT-----VLPNRVGLPINOREILVEL 52
DB 38 PKQYPIINFTTAGATVQSNTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINOREILVEL 97
QY 53 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
DB 98 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 157
QY 113 YDRLEQLAGNLRNIEIENGNGPLEEALISALYYSTGGTQPLTLARSFFIICIMISEAARFQ 172
DB 158 YDRLEQLAGNLRNIEIENGNGPLEEALISALYYSTGGTQPLTLARSFFIICIMISEAARFQ 217
QY 173 YIEGEMRTRIRYNRS 188
DB 218 YIEGEMRTRIRYNRS 233
RESULT 8
ID AAP70838
XX AAP70838 standard; protein; 332 AA.
XX AC AAP70838;
XX DT 25-MAR-2003 (updated)
XX DT 18-FEB-1991 (first entry)
XX DE Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
XX DE A protein encoded by PRA123.
XX KW Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
XX plant toxin.
XX OS Ricinus communis.
XX FH Key
XX FT Region
XX FT Location/Qualifiers
XX FT 1..32
XX FT /note="Leader"
XX FT 33..302

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FT FT /note="A-chain"
FT FT 315..332
FT FT /note="B-chain"
XX EP237676-A.
XX PD 23-SEP-1987.
XX PF 13-NOV-1986; 86EP-0308877.
XX PR 07-MAR-1986; 86US-0837583.
XX PA (CETU ) CETUS CORP.
XX PA (CHIR ) CHIRON CORP.
XX PI Piatak M;
XX WPI; 1987-265177/38.
XX DR N-PSDB; AAN70519.
XX PT New non-glycosylated ricin precursor and toxin etc. - are prepd.
XX by recombinant DNA procedures with specific isolation steps for
XX purer and soluble prods.
XX PS Disclosure; Fig 1; 112pp; English.
XX CC The full-length sequences encoding ricin A (AAN70520), ricin D
XX (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor
XX form were obt'd. using messenger RNA to obtain a cDNA library, and
XX then probing the library to retrieve the desired cDNA inserts. The
XX library was probed using the 35-mer given in AAN70514. Figure 4 (see
XX AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three
XX plasmids contg. cDNA inserts obt'd. by probing a cDNA library for
XX sequences encoding ricin B using the probe in AAN70517. The cDNA
XX inserts can be placed into expression vectors. Site-directed
XX mutagenesis may be used to place an ATG start codon and a HindIII
XX site at the beginning of the mature protein (see AAN70518). The
XX coding sequences of the inserts can be ligated into expression
XX vectors contg. the PhoA promoter-operator and leader sequence
XX (AAN70523) and suitable retroregulators.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 332 AA;
    Query Match 97.5%; Score 941; DB 8; Length 332;
    Best Local Similarity 94.9%; Pred. No. 1.4e-92;
    Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFTTAGATVQSNTNFIRAVRGRLT-----VLPNRVGLPINOREILVEL 52
DB 38 PKQYPIINFTTAGATVQSNTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINOREILVEL 97
QY 53 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
DB 98 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 157
QY 113 YDRLEQLAGNLRNIEIENGNGPLEEALISALYYSTGGTQPLTLARSFFIICIMISEAARFQ 172
DB 158 YDRLEQLAGNLRNIEIENGNGPLEEALISALYYSTGGTQPLTLARSFFIICIMISEAARFQ 217
QY 173 YIEGEMRTRIRYNRS 188
DB 218 YIEGEMRTRIRYNRS 233
RESULT 9
ID AAP95639
XX AAP95639 standard; protein; 332 AA.
XX AC AAP95639;
XX DT 25-MAR-2003 (updated)
XX DT 31-OCT-2002 (updated)

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DT 13-AUG-1990 (first entry)
 XX Ricin A encoded by insert from plasmid pRA123.
 XX Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.
 XX Ricinus communis.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..35
 FT /label= leader sequence
 FT Peptide 36..302
 FT /label=A-chain
 FT Peptide 303..314
 FT /label=linker
 FT Peptide 315..332
 FT /label=B-chain
 XX EP335476-A.
 PN
 XX
 XX 04-OCT-1989.
 PD
 XX
 XX 19-JAN-1989; 89EP-0201162.
 PF
 XX
 XX 08-FEB-1984; 84US-0578115.
 PR
 XX 08-FEB-1984; 84US-0578121.
 PR
 XX 08-FEB-1984; 84US-0578122.
 PR
 XX 07-SEP-1984; 84US-0648759.
 PR
 XX 20-SEP-1984; 84US-0653515.
 PR
 XX
 XX (CETU) CETUS CORPORATION.
 PA
 XX
 XX Gelfand D, Lawyer FC, Horn G, Greenfield L, Nitecki D, Kaplan D;
 PI Platak NJ;
 PI
 XX WPI; 1989-286959/40.
 DR N-PSDB; AAN91281.
 DR
 XX Recombinant vectors expressing ricin chains or diphtheria toxin -used for
 PT prodn. of new immunotoxin conjugates with monoclonal antibodies, having
 PT high cell specificity and good extracellular stability.
 PT
 XX Disclosure; Fig 14; 54pp; English.
 PS
 XX Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for
 CC ricin A, as well as codons for 12 AAs joining the A to the B chain.
 CC Following modification for ease of manipulation the plasmid was used to
 CC construct expression vectors which express the conjugates in
 CC host cells.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 332 AA;
 SQ
 Query Match 97.5%; Score 941; DB 10; Length 332;
 Best Local Similarity 94.9%; Pred. NO. 1.4e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVREHIVLPNRVGLPINQRFILVEL 97
 QY 53 SNHAELSVTLALDVNTAVYVGRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 112
 DB 98 SNHAELSVTLALDVNTAVYVGRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 157
 QY 113 YDRLEQLAGNIRELNGNPLEEAIISALYYSTGTOPLTARSFFIICMISEARFQ 172
 DB 158 YDRLEQLAGNIRELNGNPLEEAIISALYYSTGTOPLTARSFFIICMISEARFQ 217

QY 173 YIEGEMRTRIRYNRRS 188
 DB 218 YIEGEMRTRIRYNRRS 233
 RESULT 10
 AAR70827
 ID AAR70827 standard; Protein; 554 AA.
 XX
 AC AAR70827;
 XX
 DT 25-MAR-2003 (updated)
 DT 31-AUG-1995 (first entry)
 XX
 DE Anti-cataract immunotoxin.
 XX
 KW Immunotoxin; heavy chain; light chain; variable region; antibody;
 KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
 KW pHB19; 4197X; monoclonal antibody; MAB.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT /label= Sig_peptide
 FT /note= "phoA signal sequence"
 FT Domain 28..145
 FT /label= HEAVY
 FT Peptide 148..166
 FT /note= "MAB 4197X heavy chain"
 FT /label= LINKER
 FT Domain 169..274
 FT /label= LIGHT
 FT /note= "MAB 419X light chain"
 FT Domain 276..544
 FT /label= RICIN-A
 FT Peptide 549..554
 FT /label= TAG
 FT /note= "hexa-histidine tail"
 XX
 PN MO9503828-A1.
 XX
 PD 09-FEB-1995.
 XX
 XX 15-JUL-1994; 94WO-US07919.
 PF
 XX
 XX 02-AUG-1993; 93US-0101329.
 PR
 XX (HOUS-) HOUSTON BIOTECHNOLOGY INC.
 PA
 XX Gould RM, Kelleher PJ, Wallace TL, Wood MS;
 PI
 XX WPI; 1995-082036/11.
 DR N-PSDB; AAQ85386.
 DR
 XX New single chain immuno:toxin - binds specifically to epithelial
 PT cells, for inhibiting development of sec. cataracts after
 PT extra:capsular cataract extraction.
 PT
 XX Disclosure; Fig.4; 68pp; English.
 PS
 XX
 CC The immunotoxin given in AAR70827 comprises the heavy and light chain
 CC variable regions of anti-lens epithelium IgG3 MAb 4197X linked to
 CC ricin-A and a hexa-histidine tag. The DNA construct encoding the
 CC immunotoxin was expressed from pHB19 in E. coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 554 AA;
 SQ
 Query Match 97.5%; Score 941; DB 16; Length 554;
 Best Local Similarity 94.9%; Pred. NO. 2.7e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 Db 280 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHEIPVLPNRVGLPINQRFILVEL 339
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGFN 112
 Db 340 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGFN 399
 QY 113 YDRLEQLAGNLRNIELGNGLPLEEAIASLYYYSTGGTQTLPTLARSFIICQMISEAARFQ 172
 Db 400 YDRLEQLAGNLRNIELGNGLPLEEAIASLYYYSTGGTQTLPTLARSFIICQMISEAARFQ 459
 QY 173 YIEGEMRTRIRYNRRS 188
 Db 460 YIEGEMRTRIRYNRRS 475

RESULT 11
 AAP90079
 ID AAP90079 standard; protein; 562 AA.
 XX AC AAP90079;
 XX DT 25-MAR-2003 (updated)
 XX DT 01-NOV-1989 (first entry)
 XX DE Ricin D.
 XX DE Ricin D; Ricinus communis; castor beans; Zanicariensis variety;
 KW modified; lectin binding removed; reduced cell binding
 XX OS Ricinus communis (castor beans).
 XX PN W08904839-A.
 XX PD 01-JUN-1989.
 XX PF 23-NOV-1988; 88WO-US04238.
 XX PR 24-NOV-1987; 87US-0124735.
 XX PA (GEMY) GENETICS INST INC.
 XX PI Brown EL, Jones S;
 XX WPI; 1989-178366/24.
 XX DR N-PSDB; AAN90068.
 XX PT Modified ricin molecules and toxin conjugates
 PT - in which the lectin binding function of the B chain
 PT is removed or diminished to reduce cell binding.
 XX PS Disclosure; fig 1; 51pp; English.
 XX CC Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
 CC of DNA from Ricinus communis, Zanicariensis variety. Patent
 CC discloses many modifications of ricin in which the lectin binding
 CC function of the B chain is diminished or removed, and conjugation
 CC to toxins to eliminate cell binding.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 562 AA;

Query Match 97.5%; Score 941; DB 10; Length 562;
 Best Local Similarity 94.9%; Pred. No. 2.8e-92;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 Db 38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHEIPVLPNRVGLPINQRFILVEL 97
 QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGFN 112

Db 98 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAGFN 157
 QY 113 YDRLEQLAGNLRNIELGNGLPLEEAIASLYYYSTGGTQTLPTLARSFIICQMISEAARFQ 172
 Db 158 YDRLEQLAGNLRNIELGNGLPLEEAIASLYYYSTGGTQTLPTLARSFIICQMISEAARFQ 217
 QY 173 YIEGEMRTRIRYNRRS 188
 Db 218 YIEGEMRTRIRYNRRS 233

RESULT 12
 AAP50166
 ID AAP50166 standard; Protein; 565 AA.
 XX AC AAP50166;
 XX DT 16-OCT-1991 (first entry)
 XX DE Sequence of preprorin encoded by pRCL617.
 XX KW Toxin; anti-tumour therapy.
 XX OS Ricinus.
 XX FH Key
 FT Peptide Location/Qualifiers
 FT /label= signal 1..24
 FT Protein 25..565
 FT Region 292..303
 FT /label= links the C-terminus of the A chain and
 FT the N-terminus of the B chain
 FT Modified-site 34..36
 FT /label= N-linked glycosylation
 FT Modified-site 260..262
 FT /label= N-linked glycosylation
 FT Modified-site 398..400
 FT /label= N-linked glycosylation
 FT Modified-site 438..440
 FT /label= N-linked glycosylation
 XX EP145111-A.
 XX PN Lord JM, Roberts LM, Lamb FI;
 XX PD 19-JUN-1985.
 XX PF 13-JUL-1984; 84EP-0304801.
 XX PR 13-MAR-1984; 84GB-0006569.
 XX PR 15-JUL-1983; 83GB-0019265.
 XX PR 15-JUL-1983; 83CH-0019265.
 XX (UYWA-) UNIV WARWICK.
 XX PI Lord JM, Roberts LM, Lamb FI;
 XX WPI; 1985-148040/25.
 XX DR N-PSDB; AAN50202.
 XX PT New DNA sequences coding for ricin type plant toxin - or its
 PT mutants, and modified vectors and host microorganisms
 XX PS Disclosure; Page 30-30c; 40pp; English.
 XX CC Preprorin is the whole polypeptide encoded by AAN50202 and the DNA
 CC encoding this is claimed. Preprorin is obtained from preprorin by
 CC removal of the AA leader sequence. The linker AA sequence which is
 CC present in the precursor polypeptide is enzymatically removed in the
 CC cell to separate the A and B chains, which are joined by a
 CC disulphide bridge during the formation of the ricin molecule itself.
 CC This linker region as well as the presumptive amino terminal leader
 CC or signal sequence are not present in the sequences already
 CC published by Funatsu et al.

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XX SQ Sequence 565 AA;
Query Match 97.5%; Score 941; DB 6; Length 565;
Best Local Similarity 94.9%; Pred. No. 2.8e-92;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFNTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
DB 27 PKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVHRDIPVLPNRVGLPINQRFILVEL 86
QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
DB 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 146
QY 113 YDRLEQLAGNLRNIELGNGPLEEAISSALYYSTGTQPLTARSFIIICIMISEARFQ 172
DB 147 YDRLEQLAGNLRNIELGNGPLEEAISSALYYSTGTQPLTARSFIIICIMISEARFQ 206
QY 173 YIEGEMTRIRYNRRS 188
DB 207 YIEGEMTRIRYNRRS 222

RESULT 13
AAG78300
ID AAG78300 standard; Protein; 565 AA.
XX AC AAG78300;
XX DT 15-NOV-2001 (first entry)
XX DE Castor bean preprorin protein (SEQ ID 1).
XX KW Castor bean plant; preprorin; ricin; A chain; B chain;
XX KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
XX KW retroviral infection; anti-HIV; virucide activity; viral protease.
XX OS Ricinus communis.
XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT Protein 25..290
XX FT /label= Signal peptide
XX FT /label= Ricin_A_chain
XX FT /note= "N-glycosidase"
XX FT Peptide 291..302
XX FT /label= Linker_peptide
XX FT /note= "Cleaved during activation of ricin"
XX FT Protein 303..565
XX FT /label= Ricin_B_chain
XX FT /note= "Galactose/N-acetylgalactosamine-binding lectin"
XX PN WO200160393-A1.
XX PD 23-AUG-2001.
XX PF 15-FEB-2001; 2001WO-US05282.
XX PR 16-FEB-2000; 2000US-0182759.
XX PA (BECH-) BECHTEL BWXT IDAHO LLC.
XX PI Keener WK, Ward TE;
XX WP1; 2001-581908/65.
XX DR N-PSDB; AAI64137.
XX Novel composition comprising toxin e.g., ricin based antiviral compound
XX FT useful for treating viral infections such as human immunodeficiency
XX FT virus infection.
XX PS Disclosure; Page 47-50; 66pp; English.

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XX The sequence relates to preprorin protein encoded by the DNA sequence
XX given in AAI64137. The invention relates to a novel toxin (e.g., ricin)
XX based antiviral agent which is toxic to virus-infected cells, but
XX non-toxic to uninfected cells. The invention has anti-HIV and virucide
XX activities. Its mechanism of action is through inactivation of cellular
XX ribosomes and enhancement of binding of the antiviral agent to galactose
XX residues on cell surfaces, and its cellular internalisation. The
XX invention is useful for treating human immunodeficiency virus infection
XX and other viral infections, especially retroviral infections. The
XX antiviral agent is activated in viral particles or early-stage infected
XX cells, killing the cells upon infection and effectively preventing the
XX integration of the viral genome into the host genome thereby preventing
XX the latency/rebound problem. The agent enters all HIV susceptible cells,
XX and not just cells known to act as host cells for the virus. The
XX antiviral agent remains inert in a cell until degraded in it, unless the
XX cell is infected with the virus, where the viral protease activates it.
XX SQ Sequence 565 AA;
Query Match 97.5%; Score 941; DB 22; Length 565;
Best Local Similarity 94.9%; Pred. No. 2.8e-92;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFNTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
DB 27 PKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVHRDIPVLPNRVGLPINQRFILVEL 86
QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112
DB 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 146
QY 113 YDRLEQLAGNLRNIELGNGPLEEAISSALYYSTGTQPLTARSFIIICIMISEARFQ 172
DB 147 YDRLEQLAGNLRNIELGNGPLEEAISSALYYSTGTQPLTARSFIIICIMISEARFQ 206
QY 173 YIEGEMTRIRYNRRS 188
DB 207 YIEGEMTRIRYNRRS 222

RESULT 14
AAG78304
ID AAG78304 standard; Protein; 565 AA.
XX AC AAG78304;
XX DT 27-NOV-2001 (first entry)
XX DE Modified castor bean preprorin (SEQ ID 10).
XX KW Castor bean plant; preprorin; ricin; A chain; B chain;
XX KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
XX KW retroviral infection; anti-HIV; virucide; viral protease.
XX OS Chimeric - Ricinus communis
XX OS Chimeric - Human immunodeficiency virus type 2.
XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT Protein 25..565
XX FT /label= Signal_peptide
XX FT /label= Prorin
XX FT /note= "Prorin consists of the ricin A chain, a linker
XX FT peptide, and the ricin B chain. Prorin is
XX FT proteolytically cleaved between the A chain and
XX FT the linker to yield mature ricin"
XX FT Protein 25..291
XX FT /label= Ricin_A_chain
XX FT /note= "N-glycosidase"
XX FT Peptide 292..303
XX FT /label= Linker_peptide
XX FT Cleavage-site 296..297

```

FT Protein /label= HIV_protease_cleavage_site
FT 344..565
FT /label= Ricin B chain
FT /note= "Galactose/N-acetylgalactosamine-binding lectin"
XX PN
XX WO200160393-A1.
XX 23-AUG-2001.
XX 15-FEB-2001; 2001WO-US05282.
XX 16-FEB-2000; 2000US-0182759.
XX (BECH-) BECHTEL BMXT IDAHO LLC.
XX Keener WK, Ward TE;
XX WPI; 2001-581908/65.
XX N-PSDB; AA164145.
XX Novel composition comprising toxin e.g., ricin based antiviral compound
PT useful for treating viral infections such as human immunodeficiency
PT virus infection.
XX
XX Example 1; Page 59-63; 66pp; English.
XX The sequence relates to the amino acid sequence of a modified prepropricin
CC protein encoded by A164145. The invention relates to a novel toxin
CC (e.g. ricin) based antiviral agent which is toxic to virus-infected
CC cells, but non-toxic to uninfected cells. The invention has anti-HIV and
CC virucide activities. The agent is able to enter all HIV susceptible
CC cells, and not just cells known to act as host cells for the virus. The
CC antiviral agent remains inert in a cell unless the cell is infected
CC with the HIV virus, where the viral protease activates it. Ricin's
CC mechanism of action is through inactivation of cellular ribosomes and
CC enhancement of binding of the antiviral agent to galactose residues on
CC cell surfaces, and its cellular internalisation. The invention is useful
CC for treating human immunodeficiency virus infection and other viral
CC infections, especially retroviral infections. The antiviral agent is
CC activated in viral particles or early-stage infected cells, killing the
CC cells upon infection and effectively preventing the integration of the
CC viral genome into the host genome thereby preventing the latency/rebound
CC problem.
XX
XX Sequence 565 AA;
Query Match 97.5%; Score 941; DB 22; Length 565;
Best Local Similarity 94.9%; Pred. No. 2.8e-92;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 52
Db 27 PKQYPIINFTTAGATVQSYTNFIRAVRGLTGGADVRRHEIPVLPNRVGLPINQRFILVEL 86
QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGN 112
Db 87 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGN 146
QY 113 YDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQPTLARSFIICQMISEAARFQ 172
Db 147 YDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQPTLARSFIICQMISEAARFQ 206
QY 173 YIEGEMRTRIRYNRS 188
Db 207 YIEGEMRTRIRYNRS 222
RESULT 15
AAP70326
ID AAP70326 standard; Protein; 576 AA.
XX
AC AAP70326;
XX

DT 25-MAR-2003 (updated)
DT 21-MAY-1991 (first entry)
XX
DE Sequence of Ricinus communis (castor bean) Ricin toxin
DE (RT or ricin) E precursor encoded by PRT38.
XX
KW Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
KW plant toxin.
XX
OS Ricinus communis.
XX
XX Key Location/Qualifiers
FH Region 1..35
FT /note= "leader"
FT Region 36..302
FT /note= "A-chain"
FT Region 315..576
FT /note= "B-chain"
XX
PN EP237676-A.
XX
XX 23-SEP-1987.
XX
XX 13-NOV-1986; 86EP-0308877.
XX
XX 07-MAR-1986; 86US-0837583.
XX (CETU) CETUS CORP.
XX (CHIR) CHIRON CORP.
XX
XX Piatak M;
XX
XX WPI; 1987-265177/38.
XX N-PSDB; AAN70526.
XX
XX New non-glycosylated ricin precursor and toxin etc. - are prepd.
XX by recombinant DNA procedures with specific isolation steps for
XX purer and soluble prods.
XX
XX Disclosure; Fig 14(1-2); 112pp; English.
XX
XX The full length sequences encoding ricin A (AAN70520), ricin D
CC (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor
CC form were obtained, using the messenger RNA to obtain a cDNA library, and
CC then probing the library to retrieve the desired cDNA inserts. The
CC library was probed using the 35-mer given in AAN70514. Figure 4 (see
CC AAN70520, AAN70521, AAN70522), shows the nucleotide sequences of three
CC plasmids containing cDNA inserts obtained by probing a cDNA library
CC for sequences encoding ricin B using the probe in AAN70517. The cDNA
CC inserts can be placed into expression vectors. Site-directed
CC mutagenesis may be used to place an ATG start codon and a HindIII
CC site at the beginning of the mature protein, (see AAN70518). The
CC coding sequences of the inserts can be ligated into expression
CC vectors containing the PhOA promoter-operator and leader sequence
CC (AAN70523) and suitable retroregulators.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 576 AA;
Query Match 97.5%; Score 941; DB 8; Length 576;
Best Local Similarity 94.9%; Pred. No. 2.9e-92;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 52
Db 38 PKQYPIINFTTAGATVQSYTNFIRAVRGLTGGADVRRHEIPVLPNRVGLPINQRFILVEL 97
QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGN 112
Db 98 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGN 157
QY 113 YDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQPTLARSFIICQMISEAARFQ 172

Db 158 YDRLEQLAGNLRNIELGNGPLEEASALYYSTGGTQPLTARSFFICIQMISEARFQ 217

Qy 173 YIEGEMTRIRYNRRS 188

|||||

Db 218 YIEGEMTRIRYNRRS 233

Search completed: February 10, 2004, 16:22:28
Job time : 33.0534 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:20 ; Search time 33.9288 Seconds
(without alignments)
930.966 Million cell updates/sec

Title: US-10-083-336A-5

Perfect score: 1025
Sequence: 1 MIFPKQYPIINFTAGATVQ.....ARFQVIEGEMTRIRYNRRS 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_19Jun03.*

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1020	99.5	267	14	AAAR37290
2	1020	99.5	267	16	Ricin A chain. Un
3	1020	99.5	290	18	Ricin A-chain ribo
4	1020	99.5	290	18	Ricin A-chain ribo
5	1020	99.5	332	8	AAAP70097
6	1020	99.5	332	8	AAAP70838
7	1020	99.5	332	10	AAAP95639
8	1020	99.5	554	16	AAAR70827
9	1020	99.5	562	10	AAAP90079

10	1020	99.5	565	22	AAAG78304	Modified castor be
11	1020	99.5	576	8	AAAP70326	Sequence of Ricinu
12	1020	99.5	576	18	AAW25787	Castor bean ricin.
13	1020	99.5	576	20	AAAY55892	Castor bean ricin
14	1020	99.5	576	21	AAAY78592	Ricinus communis r
15	1020	99.5	576	22	AAAG78301	Ricinus communis r
16	1020	99.5	576	22	AAAG78302	Castor bean prepro
17	1018	99.3	268	14	AAAR39570	Sequence of ricin-
18	1017	99.2	565	6	AAAP50166	Sequence of prepro
19	1017	99.2	565	22	AAAG78300	Castor bean prepro
20	1016	99.1	200	9	AAAP80164	Biosynthetic multi
21	1015	99.0	534	14	AAAR39571	Sequence of G-FIT.
22	1013	98.8	574	8	AAAP70325	Sequence of Ricinu
23	1012	98.7	565	7	AAAP60240	Preproricin. Ricl
24	1011	98.6	574	10	AAAP94793	DNA sequence of ri
25	1010	98.5	267	13	AAAR30722	Ricin A from pIC11
26	1010	98.5	267	11	AAAB19265	Amino acid sequenc
27	1009	98.4	332	11	AAAR06554	Ricin A gene produ
28	993	96.9	267	16	AAAR74176	Ricin A chain (RTA
29	987	96.3	267	14	AAAR32430	Ricin A. Syntheti
30	930.5	90.8	540	18	AAW25143	Castor oil plant a
31	930.5	90.8	540	18	AAW21706	R. communis agglut
32	796.5	77.7	534	8	AAAP70324	Sequence of Ricin
33	778	75.9	280	10	AAAP95648	Ricin agglutinin A
34	342	33.4	247	16	AAAR67359	Trichosanthin anti
35	342	33.4	247	21	AAAY69048	Amino acid sequenc
36	342	33.4	248	11	AAAR07518	Synthetic alpha-tr
37	342	33.4	248	13	AAAR25573	Mature alpha-trich
38	342	33.4	267	18	AAW25140	Trichosanthin (a r
39	342	33.4	267	18	AAW21703	Trichosanthin. Tr
40	342	33.4	289	11	AAAR07514	Trichosanthin from
41	342	33.4	289	13	AAAR25572	Trichosanthin prot
42	342	33.4	289	13	AAAR29272	Encodes chinese cu
43	342	33.4	289	14	AAAR32986	Alpha-trichosanthi
44	342	33.4	289	15	AAAR55129	Chinese cucumber a
45	342	33.4	289	18	AAW10468	

ALIGNMENTS

RESULT 1

AAAR37290
ID AAR37290 standard; protein; 267 AA.

XX AC AAR37290;

XX 25-MAR-2003 (updated)

DT 09-JAN-2003 (updated)

DT 13-SEP-1993 (first entry)

XX Ricin A chain.

XX Type II ribosome-inactivating protein; type II RIP; gelonin;
XX momordin; immunoconjugate; autoimmune disease; cell killing; toxin.

XX Unidentified.

XX WO9309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US09487.

XX 04-NOV-1991; 91US-0787567.

XX 19-JUN-1992; 92US-0901707.

XX (XOMA) XOMA CORP.

XX Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

PT Analogues of type I ribosome inactivating protein - useful as
 PT cytotoxic agents, immuno toxins for treating auto immune diseases,
 PT cancer, graft versus host disease and selective cell killing in-vivo
 XX
 PS Claim 1; Page 92; 163pp; English.
 XX
 CC The invention covers analogues of Type I RIPs. Ricin is a Type II
 CC RIP whose A chain is homologous to plant type I RIPs. The analogues
 CC of the invention have a cysteine available for intermolecular
 CC disulphide bonding at an amino acid position corresp. to a position
 CC not naturally available for bonding; the cys residue is located in
 CC the C-terminal region of the analogue between a position corresp. to
 CC amino acid 251 and the C-terminus of ricin A chain. The analogues are
 CC pref. joined via a disulphide linkage to a molecule which specifically
 CC binds to a target cell, e.g. an antibody fragment.
 CC (Updated on 09-JAN-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 267 AA;

Query Match 99.5%; Score 1020; DB 14; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.7e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINORFLLV 61
 DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINORFLLV 60
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYPFAFG 121
 DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYPFAFG 120
 QY 122 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGCTQLPTLARSFIICIMISEAAR 181
 DB 121 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGCTQLPTLARSFIICIMISEAAR 180
 QY 182 FOYIEGEMRTIRYNRRS 199
 DB 181 FOYIEGEMRTIRYNRRS 198

RESULT 2
 AAR63902
 ID AAR63902 standard; protein; 267 AA.

XX AAR63902;
 AC AAR63902;
 XX
 DT 25-MAR-2003 (updated)
 DT 27-JUL-1995 (first entry)
 XX
 DE Ricin A-chain (RTA).
 XX Ricin A chain; RTA; ribosome-inactivating proteins; RIPs;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX Ricinus communis.
 OS
 XX WO9426910-A1.
 PN
 XX
 PD 24-NOV-1994.
 XX
 PF 12-MAY-1994; 94WO-US05348.
 XX
 PR 12-MAY-1993; 93US-0064691.
 XX
 XX (XOMA) XOMA CORP.
 XX
 XX Better MD, Carroll SS, Studnicka GM, Carroll SF;
 PI
 XX WPI; 1995-006804/01.
 DR
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins
 PT

PT - which are suitable for use as components of cytotoxic
 PT therapeutic agents.

PS Example 3; Fig 1; 221pp; English.

XX
 CC AAR63902 is the ricin A chain gene product, it is analogous to the
 CC ribosome-inactivating proteins (RIPs) described in AAR63903-R63911.
 CC RIPs are the key components of cytotoxic therapeutic agents (CTAs),
 CC which include gene fusion products and immunoconjugates. CTAs may
 CC be used to selectively eliminate any cell type to which a RIP
 CC component is targeted, by the specific binding capacity of the
 CC second component of the agent. They can be used in the treatment
 CC of diseases where the elimination of a particular cell type is
 CC desired, such as autoimmune disease, cancer and graft-versus-host
 CC disease.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 267 AA;

Query Match 99.5%; Score 1020; DB 16; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.7e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINORFLLV 61
 DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINORFLLV 60
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYPFAFG 121
 DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYPFAFG 120
 QY 122 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGCTQLPTLARSFIICIMISEAAR 181
 DB 121 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGCTQLPTLARSFIICIMISEAAR 180
 QY 182 FOYIEGEMRTIRYNRRS 199
 DB 181 FOYIEGEMRTIRYNRRS 198

RESULT 3
 AAW25136
 ID AAW25136 standard; Protein; 290 AA.

XX AAW25136;
 AC AAW25136;
 XX
 DT 25-MAR-2003 (updated)
 DT 02-DEC-1997 (first entry)
 XX
 DE Ricin A-chain ribosome inhibitory protein inactive precursor.
 XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; Barley Translation Inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome.
 OS
 XX Synthetic.
 XX US5646026-A.
 PN
 XX
 PD 08-JUL-1997.
 XX
 PF 07-JUN-1995; 95US-0485286.
 XX
 PR 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 PR 07-JUN-1995; 95US-0485286.
 XX
 XX (DOWC) DOWELANCO.

XX PI Hey TD, Morgan AER, Walsh TA;
 XX DR WPI; 1997-362934/33.
 XX
 XX DNA encoding pro-ribosome inactivating proteins - inactive
 PT precursors of ribosome inactivating proteins; can be expressed in
 PT eukaryotic cells without causing cell death
 XX
 PS Claim 4; Column 91-94; 186pp; English.
 XX
 XX AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
 CC which was engineered to contain a selectively removable internal peptide
 CC linker sequence separating the alpha and beta units of the RIP. When
 CC separated the two units regain activity and are capable of inactivating
 CC eukaryotic ribosomes and hence preventing protein production. Many
 CC different RIPs may be produced with an internal linker including
 CC maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
 CC Saporin. The RIPs can be used in the construction of therapeutic
 CC toxins targeted to specific cells such as tumour cells via the
 CC attachment of a targeting polypeptide, e.g. a monoclonal antibody.
 CC A further use is in HIV therapy (see US4869903). There is interest
 CC in expressing RIP recombinantly in host eukaryotic cells, because of
 CC the capacity to provide correct post-translational processing. However,
 CC RIPs effectively inhibit protein synthesis in eukaryotic cells resulting
 CC in cell death. Since the inactive RIP proteins are not cytotoxic to
 CC eukaryotic cells, they can be recombinantly expressed in such cells and
 CC then converted to active RIP proteins.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 290 AA;
 SQ

Query Match 99.5%; Score 1020; DB 18; Length 290;
 Best Local Similarity 100.0%; Pred. No. 3e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 61
 Db 25 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 84
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 121
 Db 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 144
 QY 182 FOYIEGEMTRIRYNNRS 199
 Db 205 FOYIEGEMTRIRYNNRS 222

RESULT 4
 AAW21699
 ID AAW21699 standard; Protein; 290 AA.
 XX
 AC AAW21699;
 XX
 XX 25-MAR-2003 (updated)
 DT 26-SEP-1997 (first entry)
 XX
 XX Ricin A-chain RIP.
 XX pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
 XX
 OS Ricinus communis.
 XX
 XX Key
 FH Location/Qualifiers
 FT Region 152..162

FT
 FT
 XX
 XX
 XX US5635384-A.
 XX
 XX 03-JUN-1997.
 XX
 XX 26-JAN-1995; 95US-0378761.
 XX
 XX 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 XX
 XX (DOMC) DOWELANCO.
 XX
 XX Hey TD, Morgan AER, Walsh TA;
 DR WPI; 1997-309831/28.
 XX
 XX Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 PT internal linker sequences
 XX
 PS Claim 2; Column 91-94; 121pp; English.
 XX
 CC The sequences given in AAW21698-710 represent Ribosome Inactivating
 CC Proteins (RIP's), which may be used in the construction of the
 CC proRIP of the invention. The proRIP has a selectively removable,
 CC internal peptide linker. The precursor sequence is incapable of
 CC inactivating eukaryotic ribosomes, but can be converted by removal
 CC of the linker into a protein having alpha and beta fragments and being
 CC capable of inactivating eukaryotic ribosomes. RIPs are potent
 CC inhibitors of eukaryotic protein synthesis. They possess a highly
 CC specific N-glycosidase activity which cleaves the glycosidic bond of
 CC adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit
 CC cellular proliferation of cells, e.g. cancer cells and HIV-infected T
 CC cells. The inactive proRIP proteins make it possible to provide protein
 CC synthesis inhibitors with uses in practical and improved ways not before
 CC possible. The RIP can be used to make cytotoxic conjugates.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 290 AA;
 Query Match 99.5%; Score 1020; DB 18; Length 290;
 Best Local Similarity 100.0%; Pred. No. 3e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 61
 Db 25 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 84
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 121
 Db 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 144
 QY 122 GNYDLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAR 181
 Db 145 GNYDLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAR 204
 QY 182 FOYIEGEMTRIRYNNRS 199
 Db 205 FOYIEGEMTRIRYNNRS 222

RESULT 5
 AAP70097
 ID AAP70097 standard; protein; 332 AA.
 XX
 AC AAP70097;
 XX
 XX 09-APR-1991 (first entry)
 XX
 DE Ricin A.

/note= "Position of possible insertion of internal
 peptide linker sequence"

```

XX KW Ricin A; Met-aminopeptidase.
XX OS Escherichia coli.
XX PN EP219237-A.
XX PD 22-APR-1987.
XX PF 19-SEP-1986; 86EP-0307242.
XX PR 06-MAY-1986; 86US-0860330.
XX PR 20-SEP-1985; 85US-0778414.
XX PA (CETU ) CETUS CORP.
XX PI Benbassat A, Bauer KA, Chang S, Chang SY;
XX WPI; 1987-110172/16.
XX DR N-PSDB; AAN70152.
XX PT N-terminal methionine free proteins prodn. - by using host
XX PT transformed with vector to express a methionine-amino-peptidase
XX PS Disclosure; Fig. 4; 20pp; English.
XX CC Ricin A may be produced in a form which lacks an N-terminal Met
XX CC using Met-aminopeptidase from E.coli.
XX SQ Sequence 332 AA;
Query Match 99.5%; Score 1020; DB 8; Length 332;
Best Local Similarity 100.0%; Pred. No. 3.6e-100;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
Db 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 95
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
Db 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 155
QY 122 GNYDRLEQLAGNLRNIEELGNGLPLEEALSALYYSTGGTQPLTLARSFIIQMISEAR 181
Db 156 GNYDRLEQLAGNLRNIEELGNGLPLEEALSALYYSTGGTQPLTLARSFIIQMISEAR 215
QY 182 FOYIEGEMTRIRYNRRS 199
Db 216 FOYIEGEMTRIRYNRRS 233
RESULT 6
AAP70838
ID AAP70838 standard; protein; 332 AA.
XX AC AAP70838;
XX DT 25-MAR-2003 (updated)
XX DT 18-FEB-1991 (first entry)
XX SE Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
XX DE A protein encoded by pR123.
XX KW Lectin; toxin protein; cytotoxic; castor bean;
XX KW plant toxin.
XX OS Ricinus communis.
XX FH Key Location/Qualifiers
XX FT Region 1..32
XX FT /note="Leader"
XX FT Region 33..302

```

```

FT FT /note="A-chain"
FT FT 315..332
FT FT /note="B-chain"
XX PN EP237676-A.
XX PD 23-SEP-1987.
XX PF 13-NOV-1986; 86EP-0308877.
XX PR 07-MAR-1986; 86US-0837583.
XX PA (CETU ) CETUS CORP.
XX PA (CHIR ) CHIRON CORP.
XX PI Piatak M;
XX WPI; 1987-265177/38.
XX DR N-PSDB; AAN70519.
XX PT New non-glycosylated ricin precursor and toxin etc. - are prepd.
XX PT by recombinant DNA procedures with specific isolation steps for
XX PS purer and soluble prods.
XX PS Disclosure; Fig 1; 112pp; English.
XX CC The full-length sequences encoding ricin A (AAN70520), ricin D
XX CC (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor
XX CC form were obtd. using messenger RNA to obtain a cDNA library, and
XX CC then probing the library to retrieve the desired cDNA inserts. The
XX CC library was probed using the 35-mer given in AAN70514. Figure 4 (see
XX CC AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three
XX CC plasmids contg. cDNA inserts obtd. by probing a cDNA library for
XX CC sequences encoding ricin B using the probe in AAN70517. The cDNA
XX CC inserts can be placed into expression vectors. Site-directed
XX CC mutagenesis may be used to place an AUG start codon and a HindIII
XX CC site at the beginning of the mature protein (see AAN70518). The
XX CC coding sequences of the inserts can be ligated into expression
XX CC vectors contg. the PhOA promoter-operator and leader sequence
XX CC (AAN70523) and suitable retroregulators.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 332 AA;
Query Match 99.5%; Score 1020; DB 8; Length 332;
Best Local Similarity 100.0%; Pred. No. 3.6e-100;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
Db 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 95
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
Db 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 155
QY 122 GNYDRLEQLAGNLRNIEELGNGLPLEEALSALYYSTGGTQPLTLARSFIIQMISEAR 181
Db 156 GNYDRLEQLAGNLRNIEELGNGLPLEEALSALYYSTGGTQPLTLARSFIIQMISEAR 215
QY 182 FOYIEGEMTRIRYNRRS 199
Db 216 FOYIEGEMTRIRYNRRS 233
RESULT 7
AAP95639
ID AAP95639 standard; protein; 332 AA.
XX AC AAP95639;
XX DT 25-MAR-2003 (updated)
XX DT 31-OCT-2002 (updated)

```

DT 13-AUG-1990 (first entry)
 XX Ricin A encoded by insert from plasmid pRA123.
 DE Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.
 XX Ricinus communis.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..35
 FT /label= leader sequence
 FT Peptide 36..302
 FT /label=A-chain
 FT Peptide 303..314
 FT /label=linker
 FT Peptide 315..332
 FT /label=B-chain
 XX EP335476-A.
 XX
 PD 04-OCT-1989.
 XX
 XX 19-JAN-1989; 89EP-0201162.
 XX
 PR 08-FEB-1984; 84US-0578115.
 PR 08-FEB-1984; 84US-0578121.
 PR 09-FEB-1984; 84US-0578122.
 PR 07-SEP-1984; 84US-0648759.
 PR 20-SEP-1984; 84US-0653515.
 XX
 PA (CETU) CETUS CORPORATION.
 XX
 XX Gelfand D, Lawyer FC, Horn G, Greenfield L, Nitecki D, Kaplan D;
 PI Piatax NJ;
 XX
 DR WPI; 1989-286959/40.
 DR N-PSDB; AAN91281.
 XX
 PT Recombinant vectors expressing ricin chains or diphtheria toxin -used for
 PT prodn. of new immunotoxin conjugates with monoclonal antibodies, having
 PT high cell specificity and good extracellular stability.
 XX
 PS Disclosure; Fig 14; 54pp; English.
 XX
 CC Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for
 CC ricin A, as well as codons for 12 AAs joining the A to the B chain.
 CC Following modification for ease of manipulation the plasmid was used to
 CC construct expression vectors which express the conjugates in
 CC host cells.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 332 AA;
 Query Match 99.5%; Score 1020; DB 10; Length 332;
 Best Local Similarity 100.0%; Pred. No. 3.6e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFNTAGATVQSYNFRVAVRGRUTTGADVREHVPVLPNVRVGLPINORFIIIV 61
 DB 36 IFPKQYPIINFNTAGATVQSYNFRVAVRGRUTTGADVREHVPVLPNVRVGLPINORFIIIV 95
 QY 62 ELSNHAELSVTALDVNTAYVGVYRAGNSAYFFHPDNQDEAETHLFTDVQNRVTFAGF 121
 DB 96 ELSNHAELSVTALDVNTAYVGVYRAGNSAYFFHPDNQDEAETHLFTDVQNRVTFAGF 155
 QY 122 GNYDRLEQAGLNRENIELGNGLPFEAISALYYSTGGTQTLPLARSFICIQMISEAR 181
 DB 156 GNYDRLEQAGLNRENIELGNGLPFEAISALYYSTGGTQTLPLARSFICIQMISEAR 215

QY 182 FOYIEGEMTRIRYNRRS 199
 DB 216 FOYIEGEMTRIRYNRRS 233
 RESULT 8
 AAR70827
 ID AAR70827 standard; Protein; 554 AA.
 XX
 AC AAR70827;
 XX
 DT 25-MAR-2003 (updated)
 DT 31-AUG-1995 (first entry)
 XX
 DE Anti-cataract immunotoxin.
 XX
 KW Immunotoxin; heavy chain; light chain; variable region; antibody;
 KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
 KW PHB19; 4197X; monoclonal antibody; MAB.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT /label= Sig_peptide
 FT /note= "phoA signal sequence"
 FT Domain 28..145
 FT /label= HEAVY
 FT /note= "MAB 4197X heavy chain"
 FT Peptide 148..166
 FT /label= LINKER
 FT Domain 169..274
 FT /label= LIGHT
 FT /note= "MAB 419X light chain"
 FT Domain 276..544
 FT /label= RICIN-A
 FT Peptide 549..554
 FT /label= TAG
 FT /note= "hexa-histidine tail"
 XX
 PN WO9503828-A1.
 XX
 PD 09-FEB-1995.
 XX
 PF 15-JUL-1994; 94WO-US07919.
 XX
 PR 02-AUG-1993; 93US-0101329.
 XX
 PA (HOUS-) HOUSTON BIOTECHNOLOGY INC.
 XX
 PI Gould RM, Kelleher PJ, Wallace TL, Wood MS;
 DR WPI; 1995-082036/11.
 DR N-PSDB; AAQ85386.
 XX
 PT New single chain immuno:toxin - binds specifically to epithelial
 PT cells, for inhibiting development of sec. cataracts after
 PT extra:capsular cataract extraction.
 XX
 PS Disclosure; Fig.4; 68pp; English.
 XX
 CC The immunotoxin given in AAR70827 comprises the heavy and light chain
 CC variable regions of anti-lens epithelium 19G3 MAB 4197X linked to
 CC ricin-A and a hexa-histidine tag. The DNA construct encoding the
 CC immunotoxin was expressed from PHB19 in E. coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 554 AA;
 Query Match 99.5%; Score 1020; DB 16; Length 554;
 Best Local Similarity 100.0%; Pred. No. 7.3e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPLINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRGLPINQRFILV 61
 DB 278 IFPKQYPLINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRGLPINQRFILV 337
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYPFAFG 121
 DB 338 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYPFAFG 337
 QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASISALYYSTGGTQPLTLARSFFIICQMISEAAR 181
 DB 398 GNYDRLEQLAGNLRENIELGNGLPLEEASISALYYSTGGTQPLTLARSFFIICQMISEAAR 457
 QY 182 FOYIEGEMTRIRYNRRS 199
 DB 458 FOYIEGEMTRIRYNRRS 475
 RESULT 9
 AAP90079
 ID AAP90079 standard; protein; 562 AA.
 XX AC AAP90079;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-NOV-1989 (first entry)
 XX
 DE Ricin D.
 XX Ricin D; Ricinus communis; castor beans; Zanicbariensis variety;
 KW modified; lectin binding removed; reduced cell binding
 XX
 OS Ricinus communis (castor beans).
 XX
 PN W08904839-A.
 XX
 PD 01-JUN-1989.
 XX
 PF 23-NOV-1988; 88WO-US04238.
 XX
 PR 24-NOV-1987; 87US-0124735.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Brown EL, Jones S;
 XX
 XX WPI; 1989-178366/24.
 DR N-PSDB; AAN90068.
 XX
 PT Modified ricin molecules and toxin conjugates
 PT - in which the lectin binding function of the B chain
 PT is removed or diminished to reduce cell binding.
 XX
 PS Disclosure; fig 1; 51pp; English.
 XX
 CC Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
 CC of DNA from Ricinus communis, Zanicbariensis variety. Patent
 CC discloses many modifications of ricin in which the lectin binding
 CC function of the B chain is diminished or removed, and conjugation
 CC to toxins to eliminate cell binding.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 562 AA;

Query Match 99.5%; Score 1020; DB 10; Length 562;
 Best Local Similarity 100.0%; Pred. No. 7.4e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPLINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRGLPINQRFILV 61
 DB 36 IFPKQYPLINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRGLPINQRFILV 95
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYPFAFG 121

DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYPFAFG 155
 QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASISALYYSTGGTQPLTLARSFFIICQMISEAAR 181
 DB 156 GNYDRLEQLAGNLRENIELGNGLPLEEASISALYYSTGGTQPLTLARSFFIICQMISEAAR 215
 QY 182 FOYIEGEMTRIRYNRRS 199
 DB 216 FOYIEGEMTRIRYNRRS 233
 RESULT 10
 AAG78304
 ID AAG78304 standard; Protein; 565 AA.
 XX
 XX AAG78304;
 DT 27-NOV-2001 (first entry)
 XX
 DE Modified castor bean preprorin (SEQ ID 10).
 XX
 KW Castor bean plant; preprorin; ricin; A chain; B chain;
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
 KW retroviral infection; anti-HIV; virucide; viral protease.
 XX
 OS Chimeric - Ricinus communis
 OS Chimeric - Human immunodeficiency virus type 2.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Signal_peptide
 FT 25..565
 FT /label= Prorin
 FT /note= "Prorin consists of the ricin A chain, a linker
 FT peptide, and the ricin B chain. Prorin is
 FT proteolytically cleaved between the A chain and
 FT the linker to yield mature ricin"
 FT
 FT Protein 25..291
 FT /label= Ricin_A_chain
 FT /note= "N-glycosidase"
 FT 292..303
 FT Peptide /label= Linker_peptide
 FT
 FT Cleavage-site 296..297
 FT /label= HIV_protease_cleavage_site
 FT 304..565
 FT Protein /label= Ricin_B_chain
 FT /note= "Galactose/N-acetylgalactosamine-binding lectin"
 FT
 PN W0200160393-A1.
 XX
 PD 23-AUG-2001.
 XX
 XX 15-FEB-2001; 2001WO-US05282.
 XX
 PR 16-FEB-2000; 2000US-0182759.
 XX
 PA (BECH-) BECHTEL BWXT IDAHO LLC.
 XX
 XX Keener WK, Ward TE;
 PI WPI; 2001-581908/65.
 DR N-PSDB; AAI64145.
 XX
 XX Novel composition comprising toxin e.g., ricin based antiviral compound
 PT useful for treating viral infections such as human immunodeficiency
 PT virus infection.
 XX
 PS Example 1; Page 59-63; 66pp; English.
 XX
 CC The sequence relates to the amino acid sequence of a modified preprorin
 CC protein encoded by AAI64145. The invention relates to a novel toxin
 CC (e.g. ricin) based antiviral agent which is toxic to virus-infected

CC cells, but non-toxic to uninfected cells. The invention has anti-HIV and
 CC virucide activities. The agent is able to enter all HIV susceptible
 CC cells, and not just cells known to act as host cells for the virus. The
 CC antiviral agent remains inert in a cell unless the cell is infected
 CC with the HIV virus, where the viral protease activates it. Ricin's
 CC mechanism of action is through inactivation of cellular ribosomes and
 CC enhancement of binding of the antiviral agent to galactose residues on
 CC cell surfaces, and its cellular internalisation. The invention is useful
 CC for treating human immunodeficiency virus infection and other viral
 CC infections, especially retroviral infections. The antiviral agent is
 CC activated in viral particles or early-stage infected cells, killing the
 CC cells upon infection and effectively preventing the integration of the
 CC viral genome into the host genome thereby preventing the latency/rebound
 CC problem.

XX Sequence 565 AA;
 SQ
 Query Match 99.5%; Score 1020; DB 22; Length 565;
 Best Local Similarity 100.0%; Pred. No. 7.5e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
 Db |||||
 25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 84
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 121
 Db |||||
 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 144
 QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIICIMISEAAR 181
 Db |||||
 145 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIICIMISEAAR 204
 QY 182 FOYIEGEMRTRIRYNRRS 199
 Db |||||
 205 FOYIEGEMRTRIRYNRRS 222

RESULT 11

AAP70326

ID AAP70326 standard; Protein; 576 AA.

XX AAP70326;

XX AC

XX 25-MAR-2003 (updated)

DT 21-MAY-1991 (first entry)

XX Sequence of Ricinus communis (castor bean) Ricin toxin
 DE (RT or ricin) E precursor encoded by pRT38.
 XX

XX Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
 KW plant toxin.
 XX

OS Ricinus communis.

XX Key

XX Location/Qualifiers

XX Region

XX 1..35

XX /note= "leader"

XX Region

XX 36..302

XX /note= "A-chain"

XX Region

XX 315..576

XX /note= "B-chain"

XX EP237676-A.

XX 23-SEP-1987.

XX 13-NOV-1986;

XX 86EP-0308877.

XX 07-MAR-1986;

XX 86US-0837583.

XX (CETU) CETUS CORP.

XX (CHIR) CHIRON CORP.

XX PA

XX

PI Piatak M;

XX

XX WPI; 1987-265177/38.

XX

XX N-PSDB; AAN70526.

XX

XX New non-glycosylated ricin precursor and toxin etc. - are prepd.
 PT by recombinant DNA procedures with specific isolation steps for
 PT purer and soluble prods.

XX

XX Disclosure; Fig 14(1-2); 112pp; English.

XX

CC The full length sequences encoding ricin A (AAN70520), ricin D
 CC (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor
 CC form were obtained, using the messenger RNA to obtain a cDNA library, and
 CC then probing the library to retrieve the desired cDNA inserts. The
 CC library was probed using the 35-mer given in AAN70514. Figure 4 (see
 CC AAN70520, AAN70521, AAN70522), shows the nucleotide sequences of three
 CC plasmids containing cDNA inserts obtained by probing a cDNA library
 CC for sequences encoding ricin B using the probe in AAN70517. The cDNA
 CC inserts can be placed into expression vectors. Site-directed
 CC mutagenesis may be used to place an ATG start codon and a HindIII
 CC site at the beginning of the mature protein, (see AAN70518). The
 CC coding sequences of the inserts can be ligated into expression
 CC vectors containing the pho promoter-operator and leader sequence
 CC (AAN70523) and suitable retroregulators.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 576 AA;

SQ

Query Match 99.5%; Score 1020; DB 8; Length 576;

Best Local Similarity 100.0%; Pred. No. 7.7e-100;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
 Db |||||

36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 95
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 121
 Db |||||

96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAG 155
 QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIICIMISEAAR 181
 Db |||||

156 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIICIMISEAAR 215
 QY 182 FOYIEGEMRTRIRYNRRS 199
 Db |||||

216 FOYIEGEMRTRIRYNRRS 233

RESULT 12

AAW25787

ID AAW25787 standard; Protein; 576 AA.

XX AAW25787;

XX AC

XX 25-MAR-2003 (updated)

DT 27-MAR-1998 (first entry)

XX

XX Castorbean ricin.

XX

XX Ricin; cytotoxin; hybrid protein; cell delivery;
 KW cell binding ligand; translocation domain; diphtheria toxin B';
 KW interleukin-2; T-cell lymphoma; organ rejection; therapy.
 XX

OS Ricinus communis.

XX Key

XX Location/Qualifiers

XX Peptide

XX 1..35

XX /label= Sig_peptide

XX Protein

XX 36..302

XX /label= A-domain

XX FT

PT Peptide 303...314
 FT /label= Linker
 FT Domain 315...576
 FT /label= B-domain

PN US5668255-A.

PD 16-SEP-1997.

PF 04-AUG-1993; 93US-0102387.

PR 27-JUN-1991; 91US-0722484.

PR 07-JUN-1984; 84US-0618199.

PR 25-APR-1985; 85US-0726808.

PR 27-JUN-1991; 91US-0722484.

PR 22-DEC-1989; 89US-0456095.

PR 14-JUN-1990; 90US-0538276.

PR 04-AUG-1993; 93US-0102387.

PA (SERA-) SERAGEN INC.

PI Murphy JR;

DR WPI; 1997-470103/43.

DR N-PSDB; AAT91638.

XX New hybrid molecules for delivery of agents to cells - comprise a

XX binding domain of a cell binding ligand and a portion of a

XX translocation domain of a protein

XX Example 4; Fig 11A-B; 30pp; English.

XX This polypeptide comprises the castorbean cytotoxin, ricin.

XX DNA (see AAY5892) encoding the enzymatic A domain and a portion

XX of the A-to-B linker peptide of ricin was used to construct a

XX ricin-diphtheria toxin B'-interleukin-2 gene that was expressed in

XX E. coli. The hybrid protein can be isolated and used to treat

XX conditions involving over-production of cells bearing IL2 receptors,

XX such as certain T-cell lymphomas and organ transplant rejection

XX crises. The hybrid inactivates ribosomes in cells bearing IL2

XX receptors, resulting in cessation of protein synthesis and death of

XX target cells. Claimed hybrid proteins comprise a translocation

XX domain and a cell binding domain from e.g. a hormone, growth factor

XX or polypeptide toxin. The hybrid molecules can be used for the

XX delivery of agents (e.g. therapeutic genes, toxins, detectable

XX labels) into cells. The use of a translocation mechanism ensures

XX that the hybrid will be effective in relatively low doses, since a

XX high proportion of the substance of interest will be taken into the

XX targeted cells. The hybrid molecules can be manufactured as a

XX single hybrid recombinant protein, permitting reproducibility,

XX consistency, and the precise control of composition.

XX (Updated on 25-MAR-2003 to correct PF field.)

QY Query Match 99.5%; Score 1020; DB 18; Length 576;
 DB Best Local Similarity 100.0%; Pred. No. 7.7e-100;
 DB Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 61

QY 36 IFPKQYPIINFTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95

QY 62 ELSNHAELSVTLADVNNAVYVGRAGNSAYFFHPDQDAEATHLFTDVQRYTFAFG 121

QY 96 ELSNHAELSVTLADVNNAVYVGRAGNSAYFFHPDQDAEATHLFTDVQRYTFAFG 155

QY 122 GNYDRLEQLAGNLRENIELGNPLLEAISALYYSTGTGQTPTLARSFIICQMISEAR 181

QY 156 GNYDRLEQLAGNLRENIELGNPLLEAISALYYSTGTGQTPTLARSFIICQMISEAR 215

QY 182 FOYIEGEMTRIRYNRRS 199

QY ||||||||||||||||||

Db 216 FOYIEGEMTRIRYNRRS 233

RESULT 13

AAY55892

ID AAY55892 standard; Protein; 576 AA.

XX AC AAY55892;

XX DT 15-FEB-2000 (first entry)

XX DE Castor bean ricin toxin.

XX KW Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria;

XX KW translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus;

XX KW shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV;

XX KW cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison;

XX KW adipocyte; cancer; virus; infection; antibody.

XX OS Ricinus communis.

XX PN US5965406-A.

XX PD 12-OCT-1999.

XX PF 07-JUN-1995; 95US-0488246.

XX PR 04-AUG-1993; 93US-0102387.

XX PR 07-JUN-1984; 84US-0618199.

XX PR 27-JUN-1991; 91US-0722484.

XX PR 25-APR-1985; 85US-0726808.

XX PR 07-JUN-1985; 85US-0742554.

XX PR 22-DEC-1989; 89US-0456095.

XX PR 14-JUN-1990; 90US-0538276.

XX (SERA-) SERAGEN INC.

XX Murphy JR;

XX WPI; 1999-632431/54.

XX N-PSDB; AAZ30663.

XX Recombinant DNA molecule encoding a three part hybrid protein used in

XX the treatment of Aids and genetic deficiency diseases -

XX Example 4; Fig 11; 31pp; English.

XX The invention relates to a recombinant DNA molecule encoding a hybrid

XX protein comprising three parts: (a) the first part comprises a portion

XX of the binding domain of a cell-binding polypeptide ligand allowing the

XX hybrid protein to bind to an animal cell; (b) the second part comprises

XX a portion of a translocation domain of a naturally occurring protein

XX selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera

XX toxin, LT toxin, C3 toxin, shiga-like toxin, pertussis toxin and tetanus

XX toxin, which translocate the third part of the across the cytoplasmic

XX membrane into the cytosol of the cell; and (c) the third part comprises

XX a polypeptide entity to be introduced into the cell, which is non-native

XX to the naturally occurring protein of (b). This sequence represents the

XX Castor bean ricin toxin sequence for use in generating the hybrid of the

XX invention. The hybrid molecule enables the direction of appropriate

XX therapy to affected cells, allowing them to function properly and

XX alleviate or cure the disease. The hybrid is especially used in treating

XX genetic deficiency diseases, by delivering to affected cells an enzyme

XX supplying the missing function, to supplementing cellular levels of a

XX particular enzyme or a scarce precursor or cofactor, to directing toxins

XX or other poisons to destroy particular cells (such as adipocytes, cancer

XX cell, or virus infected-cells), to counteracting viral infections such as

XX HIV, by introducing appropriate antibodies to viral proteins. It is also

XX involved in the process of getting non-therapeutic substances such as

XX detectable labels into cells.

XX Sequence 576 AA;

Query Match 99.5%; Score 1020; DB 20; Length 576;
 Best Local Similarity 100.0%; Pred. No. 7.7e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 61
 DB 36 IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 95
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRVYTFAG 121
 DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRVYTFAG 155
 QY 122 GNYDLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQLTPLARSFIIQMISEAR 181
 DB 156 GNYDLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQLTPLARSFIIQMISEAR 215
 QY 182 FOYIEGEMTRIRYNRRS 199
 DB 216 FOYIEGEMTRIRYNRRS 233

RESULT 14
 AAY78592
 ID AAY78592 standard; Protein; 576 AA.
 AC AAY78592;
 XX

DT 05-MAY-2000 (first entry)
 DE Ricinus communis ricin protein sequence.

KW Ricin; toxin; hybrid protein; translocation domain; cell destruction;
 KW cell binding domain; Genetic deficiency disease; cell targeting; cancer;
 KW adipocyte; enzyme delivery; anti-viral; HIV.

OS Ricinus communis.

PN US6022950-A.

PD 08-FEB-2000.

PF 07-JUN-1995; 95US-0479510.

PR 07-JUN-1984; 84US-0618199.

PR 27-JUN-1991; 91US-0722484.

PR 25-APR-1985; 85US-0726808.

PR 07-JUN-1985; 85US-0742554.

PR 22-DEC-1989; 89US-0456095.

PR 14-JUN-1990; 90US-0538276.

PR 04-AUG-1993; 93US-0102387.

PA (SERA-) SERAGEN INC.

PI Murphy JR;

PS WPI: 2000-160390/14.

DR N-PSDB; AA290019.

PT New two-part hybrid protein comprising a translocation domain and a
 PT cell-binding domain, for treating genetic deficiency diseases, cancer
 PT and HIV infections -

PS Example 4; Fig 11; 32pp; English.

XX This sequence represents the Ricinus communis ricin protein sequence. The
 CC toxin can be included in the hybrid protein of the invention and used to
 CC destroy or modify the cell that the hybrid protein is targeted to. The
 CC hybrid protein comprises a first part which is a portion of the binding
 CC domain of a cell-binding ligand, effective to cause the hybrid molecule
 CC to bind to a cell of an animal. The second part comprises a portion of a
 CC translocation domain of a naturally occurring protein (e.g. the
 CC translocation domain of diphtheria toxin) the second part translocates
 CC the third part across the cytoplasmic membrane and into the cytosol of

CC the cell. The third part comprises a chemical entity to be introduced
 CC into the cell, where each of the first and third part is non-native with
 CC respect to naturally occurring protein, and the covalent bond attaching
 CC the second and third part is cleavable. The toxin represented by the
 CC present sequence can form part of the third portion of the hybrid
 CC protein. The cell binding domain binds to a specific cell and the
 CC translocation domain transfers the hybrid molecule across the cell
 CC membrane into the cytosol. The third part of the protein, linked to its
 CC translocation domain through a cleavable bond, can then carry out its
 CC function. The hybrid molecules are useful for treating genetic deficiency
 CC diseases by delivering to affected cells an enzyme supplying the missing
 CC function, to supplement cellular levels of a particular enzyme or a
 CC scarce precursor or cofactor, to direct toxins or other poisons to
 CC destroy particular cells (such as adipocytes, cancer cells, or
 CC virus-infected cells), and to counteract viral infections such as HIV by
 CC introducing into appropriate cells antibodies to viral proteins.

XX Sequence 576 AA;

SQ Query Match 99.5%; Score 1020; DB 21; Length 576;
 Best Local Similarity 100.0%; Pred. No. 7.7e-100;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 61

DB 36 IFPKQYPIINFNTAGATVQSYTNFIRAVRGRLTTGADVREHPIVLPNVRGLPINORFILV 95

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRVYTFAG 121

DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRVYTFAG 155

QY 122 GNYDLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQLTPLARSFIIQMISEAR 181

DB 156 GNYDLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQLTPLARSFIIQMISEAR 215

QY 182 FOYIEGEMTRIRYNRRS 199

DB 216 FOYIEGEMTRIRYNRRS 233

RESULT 15

AAG78301

ID AAG78301 standard; Protein; 576 AA.

AC AAG78301;

DT 15-NOV-2001 (first entry)

DE Castor bean preprorin protein (SEQ ID 2).

XX Castor bean plant; preprorin; ricin; A chain; B chain;

KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
 KW retroviral infection; anti-HIV; virucide activity; viral protease.

OS Ricinus communis.

XX Key Location/Qualifiers

FT Peptide 1..35

FT /label= Signal peptide

FT Protein 36..302

FT /label= Ricin_A_chain

FT /note= "N-glycosidase"

FT Peptide 303..314

FT /label= Linker peptide

FT /note= "Cleaved during activation of ricin"

FT Protein 315..576

FT /label= Ricin_B_chain

FT /note= "Galactose/N-acetylgalactosamine-binding lectin"

XX WO200160393-A1.

PN 23-AUG-2001.

XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:18:30 ; Search time 11.5063 Seconds
(without alignments)
731.761 Million cell updates/sec

Title: US-10-083-336A-5

Perfect score: 1025

Sequence: 1 MIFPKQPIINFTTAGATVQ.....ARFQYIEGEMKTRIRYNRRS 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1025	100.0	268	2	US-08-356-786-8
2	1025	100.0	534	2	US-08-356-786-10
3	1020	99.5	267	1	US-07-901-707-1
4	1020	99.5	267	1	US-07-988-430-1
5	1020	99.5	267	1	US-08-425-336-1
6	1020	99.5	267	1	US-08-488-113B-1
7	1020	99.5	267	1	US-08-477-484B-1
8	1020	99.5	267	1	US-08-646-360-1
9	1020	99.5	267	3	US-08-839-765-1
10	1020	99.5	267	3	US-09-136-389-1
11	1020	99.5	267	4	US-08-610-838-1
12	1020	99.5	267	5	PCT-US92-09487-1
13	1020	99.5	290	1	US-08-378-761A-27
14	1020	99.5	290	1	US-08-485-286-27
15	1020	99.5	290	6	US248606-4
16	1010	98.5	267	1	US-08-218-303-16
17	1010	98.5	267	2	US-08-338-793D-61
18	1010	98.5	267	4	US-09-538-873-1
19	930.5	90.8	540	1	US-08-378-761A-77
20	930.5	90.8	540	1	US-08-485-286-77
21	342	33.4	247	1	US-08-488-113B-6
22	342	33.4	247	1	US-08-477-484B-6
23	342	33.4	247	2	US-08-646-360-6
24	342	33.4	247	3	US-08-839-765-6
25	342	33.4	247	3	US-09-136-389-6
26	342	33.4	247	4	US-09-610-838-6
27	342	33.4	267	1	US-08-378-761A-74

ALIGNMENTS

RESULT 1
US-08-356-786-8
; Sequence 8, Application US/08356786
; Patent No. 5877305

GENERAL INFORMATION:

APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: King, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-356-786-8
Query Match 100.0%; Score 1025; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 6e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 74, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 15, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 3, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 2, Appl

QY 1 MIFPKQYPIINFTAGATVQSYNFIKAVRGLTTGADVREHIEIPVLPNVRVGLPINQRFIL 60
DB 1 MIFPKQYPIINFTAGATVQSYNFIKAVRGLTTGADVREHIEIPVLPNVRVGLPINQRFIL 60
QY 61 VELSNAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDVQNRVTFAP 120
DB 61 VELSNAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDVQNRVTFAP 120
QY 121 GGNDRLEQLAGNLRENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAA 180
DB 121 GGNDRLEQLAGNLRENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAA 180
QY 181 RFQYIEGEMTRIRYNRS 199
DB 181 RFQYIEGEMTRIRYNRS 199

RESULT 2

US-08-356-786-10

; Sequence 10, Application US/08356786

; Patent No. 5877305

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: King, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer

; NUMBER OF INVENTION: Marker

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,786

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/831,967

; FILING DATE: 06-FEB-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Pitcher, Edmund R.

; REGISTRATION NUMBER: 27,829

; REFERENCE/DOCKET NUMBER: CRP-053

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 534 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-356-786-10

Query Match 100.0%; Score 1025; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.7e-111;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPKQYPIINFTAGATVQSYNFIKAVRGLTTGADVREHIEIPVLPNVRVGLPINQRFIL 60
DB 3 MIFPKQYPIINFTAGATVQSYNFIKAVRGLTTGADVREHIEIPVLPNVRVGLPINQRFIL 62
QY 61 VELSNAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDVQNRVTFAP 120

DB 63 VELSNAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDVQNRVTFAP 122
QY 121 GGNDRLEQLAGNLRENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAA 180
DB 123 GGNDRLEQLAGNLRENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAA 182
QY 181 RFQYIEGEMTRIRYNRS 199
DB 183 RFQYIEGEMTRIRYNRS 201

RESULT 3

US-07-901-707-1

; Sequence 1, Application US/07901707

; Patent No. 5376546

; GENERAL INFORMATION:

; APPLICANT: Bernhard, Susan L.

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Steve F.

; APPLICANT: Lane, Julie A.

; TITLE OF INVENTION: Materials Comprising and Methods of

; NUMBER OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/901,707

; FILING DATE: 19920619

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5376546and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27129/30910

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750

; TELEFAX: (312) 984-5750

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 267 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-901-707-1

Query Match 99.5%; Score 1020; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.3e-111;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFTAGATVQSYNFIKAVRGLTTGADVREHIEIPVLPNVRVGLPINQRFILV 61
DB 1 IFPKQYPIINFTAGATVQSYNFIKAVRGLTTGADVREHIEIPVLPNVRVGLPINQRFILV 60
QY 62 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDVQNRVTFAP 121
DB 61 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDVQNRVTFAP 120
QY 122 GGNDRLEQLAGNLRENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAA 181

Db 121 GNYDRLEQAGNLENIELGNGLPLEEASALYYSTGTQTLPTLARSFIICIMISEAAR 180
 QY 182 FOYIEGEMTRIRYNRRS 199
 Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 4

US-07-988-430-1
 ; Sequence 1, Application US/07988430
 ; Patent No. 5416202
 ; GENERAL INFORMATION:
 ; APPLICANT: Bernhard, Susan L.
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Lane, Julie A.
 ; APPLICANT: Lei, Shau-Ping
 ; TITLE OF INVENTION: Materials Comprising and Methods of
 ; Preparation and Use for Ribosome-Inactivating Proteins
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Bicknell
 ; STREET: Two First National Plaza, 20 South Clark
 ; STREET: Street
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/988,430
 ; FILING DATE: 19921209
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5416202and, Greta E.
 ; REGISTRATION NUMBER: 35302
 ; REFERENCE/DOCKET NUMBER: 31133
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 346-5750
 ; TELEFAX: (312) 984-9740
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 267 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-988-430-1

Query Match 99.5%; Score 1020; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.3e-111; Indels 0; Gaps 0;
 Matches 198; Conservative 0; Mismatches 0;
 QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVREHLPVLNVRVGLPINQRFILV 61
 Db 1 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVREHLPVLNVRVGLPINQRFILV 60
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 121
 Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 120

QY 122 GNYDRLEQAGNLENIELGNGLPLEEASALYYSTGTQTLPTLARSFIICIMISEAAR 181
 Db 121 GNYDRLEQAGNLENIELGNGLPLEEASALYYSTGTQTLPTLARSFIICIMISEAAR 180
 QY 182 FOYIEGEMTRIRYNRRS 199
 Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 5

US-08-425-336-1
 ; Sequence 1, Application US/08425336
 ; Patent No. 5621083
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; TITLE OF INVENTION: Proteins
 ; NUMBER OF SEQUENCES: 140
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/425,336
 ; FILING DATE: 18-APR-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Thomas C.
 ; REGISTRATION NUMBER: P-36,989
 ; REFERENCE/DOCKET NUMBER: 31394
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6300
 ; TELEFAX: 312/474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 267 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-425-336-1

Query Match 99.5%; Score 1020; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.3e-111; Indels 0; Gaps 0;
 Matches 198; Conservative 0; Mismatches 0;
 QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVREHLPVLNVRVGLPINQRFILV 61
 Db 1 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVREHLPVLNVRVGLPINQRFILV 60
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 121
 Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 120
 QY 122 GNYDRLEQAGNLENIELGNGLPLEEASALYYSTGTQTLPTLARSFIICIMISEAAR 181

Db 121 GNYDRLEQLAGNLRNIELGNGPLEEAI S A L Y Y Y T G T Q L P T L A R S F I I C I O M I S E A A R 180
QY 182 FOYIEGEMTRIRYNRRS 199
Db 181 FOYIEGEMTRIRYNRRS 198
RESULT 6
US-08-488-113B-1
: Sequence 1, Application US/08488113B
: Patent No. 5744580
: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: APPLICANT: Carroll, Stephen F.
: APPLICANT: Studnika, Gary M.
: TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
: TITLE OF INVENTION: Proteins
: NUMBER OF SEQUENCES: 169
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McAndrews, Held & Malloy, Ltd.
: STREET: 500 West Madison Street, 34th floor
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60661
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/488,113B
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/425,336
: FILING DATE: 18-APR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/064,691
: FILING DATE: 12-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/988,430
: FILING DATE: 09-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/901,707
: FILING DATE: 19-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/787,567
: FILING DATE: 04-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: McNicholas, Janet M.
: REGISTRATION NUMBER: 32,918
: REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/707-8889
: TELEFAX: 312/707-9155
: TELEX: 650 388-1248
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 267 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-488-113B-1
Query Match 99.5%; Score 1020; DB 1; Length 267;
Best Local Similarity 100.0%; Pred.No. 2.3e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IFPKQYPIINTTAGATVQSYTNFIRAVRGLTGTGADVRHEIPVLPNRVGLPINQRFILV 61
Db 1 IFPKQYPIINTTAGATVQSYTNFIRAVRGLTGTGADVRHEIPVLPNRVGLPINQRFILV 60

QY 62 ELSNHAELSVTLALDVNTNAYVVGYRAGNSAYFFHPDNQEDAEAI TH LFTDVQNRYYTFAFG 121
Db 61 ELSNHAELSVTLALDVNTNAYVVGYRAGNSAYFFHPDNQEDAEAI TH LFTDVQNRYYTFAFG 120
QY 122 GNYDRLEQLAGNLRNIELGNGPLEEAI S A L Y Y Y T G T Q L P T L A R S F I I C I O M I S E A A R 181
Db 121 GNYDRLEQLAGNLRNIELGNGPLEEAI S A L Y Y Y T G T Q L P T L A R S F I I C I O M I S E A A R 180
QY 182 FOYIEGEMTRIRYNRRS 199
Db 181 FOYIEGEMTRIRYNRRS 198
RESULT 7
US-08-477-484B-1
: Sequence 1, Application US/08477484B
: Patent No. 5756699
: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: APPLICANT: Carroll, Stephen F.
: APPLICANT: Studnika, Gary M.
: TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
: TITLE OF INVENTION: Proteins
: NUMBER OF SEQUENCES: 169
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McAndrews, Held & Malloy, Ltd.
: STREET: 500 West Madison Street, 34th floor
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60661
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,484B
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/425,336
: FILING DATE: 18-APR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/064,691
: FILING DATE: 12-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/988,430
: FILING DATE: 09-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/901,707
: FILING DATE: 19-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/787,567
: FILING DATE: 04-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: McNicholas, Janet M.
: REGISTRATION NUMBER: 32,918
: REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/707-8889
: TELEFAX: 312/707-9155
: TELEX: 650 388-1248
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 267 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-477-484B-1
Query Match 99.5%; Score 1020; DB 1; Length 267;

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Best Local Similarity 100.0%; Pred. No. 2.3e-111; Mismatches 0; Indels 0; Gaps 0;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINORFILV 61
Db 1 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINORFILV 60
QY 62 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDQVQRYTFAPG 121
Db 61 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDQVQRYTFAPG 120
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIICQMISEAAR 181
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIICQMISEAAR 180
QY 182 FOYIEGEMTRIRYNRRS 199
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 8
US-08-646-360-1
; Sequence 1, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-360-1

Query Match 99.5%; Score 1020; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.3e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINORFILV 61
Db 1 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINORFILV 60
QY 62 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDQVQRYTFAPG 121
Db 61 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDQVQRYTFAPG 120
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIICQMISEAAR 181
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIICQMISEAAR 180
QY 182 FOYIEGEMTRIRYNRRS 199
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 9
US-08-839-765-1
; Sequence 1, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:

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TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-1

Query Match 99.5%; Score 1020; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.3e-111; Indels 0; Gaps 0;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 61
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
QY 62 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
DB 61 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
QY 122 GNYDRLEQLAGNLENELGNPLEEASALYYSTGTLPTLARSFIICIQMISEAAR 181
DB 121 GNYDRLEQLAGNLENELGNPLEEASALYYSTGTLPTLARSFIICIQMISEAAR 180
QY 182 FOYIEGEMRTRIRYNRS 199
DB 181 FOYIEGEMRTRIRYNRS 198

RESULT 10

US-09-136-389-1
Sequence 1, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-1

Query Match 99.5%; Score 1020; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.3e-111; Indels 0; Gaps 0;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 61
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
QY 62 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
DB 61 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
QY 122 GNYDRLEQLAGNLENELGNPLEEASALYYSTGTLPTLARSFIICIQMISEAAR 181
DB 121 GNYDRLEQLAGNLENELGNPLEEASALYYSTGTLPTLARSFIICIQMISEAAR 180
QY 182 FOYIEGEMRTRIRYNRS 199
DB 181 FOYIEGEMRTRIRYNRS 198

RESULT 11

US-09-610-838-1
Sequence 1, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348


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; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70-P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-610-838-1

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Query Match          99.5%; Score 1020; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.3e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 1PPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 61
Db 1 1PPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 60

QY 62 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121
Db 61 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 120

QY 122 GNYDRLEQLAGNLRENIELGNGLPEEALSALYYSTGGTQLPTLARSFIIQIMISEAR 181
Db 121 GNYDRLEQLAGNLRENIELGNGLPEEALSALYYSTGGTQLPTLARSFIIQIMISEAR 180

QY 182 FOYIEGEMRTRIRYNRRS 199
Db 181 FOYIEGEMRTRIRYNRRS 198

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RESULT 12
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-09487-1

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Query Match          99.5%; Score 1020; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.3e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 1PPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 61
Db 1 1PPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 60

QY 62 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121
Db 61 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 120

QY 122 GNYDRLEQLAGNLRENIELGNGLPEEALSALYYSTGGTQLPTLARSFIIQIMISEAR 181
Db 121 GNYDRLEQLAGNLRENIELGNGLPEEALSALYYSTGGTQLPTLARSFIIQIMISEAR 180

QY 182 FOYIEGEMRTRIRYNRRS 199
Db 181 FOYIEGEMRTRIRYNRRS 198

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RESULT 13
US-08-378-761A-27
; Sequence 27, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-761A-27

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Query Match      99.5%; Score 1020; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 2.6e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRLHEIPVLPNVRGLPINQRFILV 61
Db      25  IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRLHEIPVLPNVRGLPINQRFILV 84

QY      62  ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 121
Db      85  ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 144

QY      122  GNYDRLEQLAGNRENIELNGNPLEEASALYYSTGGTQTLPTLARSFIICQMISEAAR 181
Db      145  GNYDRLEQLAGNRENIELNGNPLEEASALYYSTGGTQTLPTLARSFIICQMISEAAR 204

QY      182  FQYIEGEMTRIRYNRRS 199
Db      205  FQYIEGEMTRIRYNRRS 222

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RESULT 14
US-08-485-286-27
; Sequence 27, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-286-27

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Query Match      99.5%; Score 1020; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 2.6e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRLHEIPVLPNVRGLPINQRFILV 61
Db      25  IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRLHEIPVLPNVRGLPINQRFILV 84

QY      62  ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 121
Db      85  ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 144

QY      122  GNYDRLEQLAGNRENIELNGNPLEEASALYYSTGGTQTLPTLARSFIICQMISEAAR 181
Db      145  GNYDRLEQLAGNRENIELNGNPLEEASALYYSTGGTQTLPTLARSFIICQMISEAAR 204

QY      182  FQYIEGEMTRIRYNRRS 199
Db      205  FQYIEGEMTRIRYNRRS 222

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RESULT 15
5248606-4
; Patent No. 5248606
; APPLICANT: WALSH, TERENCE A; HEY, TIMOTHY D; MORGAN,
; ALICE E.R.
; TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND
; ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATION
; NUMBER OF SEQUENCES: 49
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/535,636
; FILING DATE: 11-JUN-1990
; SEQ ID NO: 4
; LENGTH: 290
5248606-4

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Query Match      99.5%; Score 1020; DB 6; Length 290;
Best Local Similarity 100.0%; Pred. No. 2.6e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRLHEIPVLPNVRGLPINQRFILV 61
Db      25  IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRLHEIPVLPNVRGLPINQRFILV 84

QY      62  ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 121
Db      85  ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 144

QY      122  GNYDRLEQLAGNRENIELNGNPLEEASALYYSTGGTQTLPTLARSFIICQMISEAAR 181
Db      145  GNYDRLEQLAGNRENIELNGNPLEEASALYYSTGGTQTLPTLARSFIICQMISEAAR 204

QY      182  FQYIEGEMTRIRYNRRS 199
Db      205  FQYIEGEMTRIRYNRRS 222

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Sun Feb 15 07:29:58 2004

us-10-083-336a-5.rai

Page 9

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 Copyright (c) 1993 - 2004 Compugen Ltd.
 OM protein - protein search, using sw model
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 (without alignments)
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 Perfect score: 1025
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 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1025	100.0	199	12	US-10-083-336A-5
2	1025	100.0	200	12	US-10-083-336A-10
3	1020	99.5	198	12	US-10-083-336A-3
4	1020	99.5	267	12	US-10-127-890-1
5	1020	99.5	576	12	US-10-083-336A-1
6	1010	98.5	198	12	US-10-083-336A-7
7	1010	98.5	267	12	US-10-282-935-1
8	1010	98.5	267	12	US-10-440-796-1
9	956	93.3	189	12	US-10-083-336A-6
10	956	93.3	190	12	US-10-083-336A-11
11	951	92.8	188	12	US-10-083-336A-4
12	941	91.8	188	12	US-10-083-336A-8
13	934.5	91.2	185	12	US-10-083-336A-9
14	748	73.0	179	12	US-10-083-336A-2
15	342	33.4	247	10	US-09-792-793A-39

16	342	33.4	247	12	US-10-127-890-6
17	342	33.4	247	12	US-10-375-209A-39
18	342	33.4	289	12	US-10-280-679B-4
19	323.5	31.6	251	12	US-10-282-935-3
20	323.5	31.6	251	12	US-10-440-796-3
21	312	30.4	247	10	US-09-792-793A-34
22	312	30.4	247	12	US-10-375-209A-34
23	279	27.2	263	12	US-10-127-890-4
24	277	27.0	263	12	US-10-127-890-7
25	276	26.9	252	9	US-09-347-064-2
26	276	26.9	252	9	US-09-347-064-8
27	267.5	26.1	248	12	US-10-127-890-5
28	246.5	24.0	251	12	US-10-127-890-110
29	246.5	24.0	251	12	US-10-127-890-111
30	245.5	24.0	251	12	US-10-127-890-101
31	244.5	23.9	251	12	US-10-127-890-99
32	243.5	23.9	251	12	US-10-127-890-107
33	243.5	23.8	251	12	US-10-127-890-100
34	243.5	23.8	251	12	US-10-127-890-106
35	242.5	23.7	251	9	US-09-765-527-247
36	242.5	23.7	251	12	US-10-127-890-2
37	242.5	23.7	251	12	US-10-127-890-102
38	242.5	23.7	251	12	US-10-127-890-103
39	242.5	23.7	251	12	US-10-127-890-104
40	242.5	23.7	251	12	US-10-127-890-105
41	242.5	23.7	316	12	US-10-074-596-1
42	242.5	23.7	507	12	US-10-074-596-11
43	241.5	23.6	251	12	US-10-127-890-109
44	241.5	23.6	293	9	US-09-765-527-259
45	241.5	23.6	309	9	US-09-765-527-253

ALIGNMENTS

RESULT 1

US-10-083-336A-5
 ; Sequence 5, Application US/10083336A
 ; Publication NO. US20030181865A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olson, Mark A
 ; APPLICANT: Millard, Charles B
 ; APPLICANT: Byrne, Michael P
 ; APPLICANT: Wannemacher, Robert W
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
 ; FILE REFERENCE: P67452US0 (RIID 01-58)
 ; CURRENT APPLICATION NUMBER: US/10/083,336A
 ; CURRENT FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; TYPE: PR1
 ; ORGANISM: Ricinus communis
 ; US-10-083-336A-5

Query Match	100.0%	Score 1025;	DB 12;	Length 199;
Best Local Similarity	100.0%	Pred. No. 1.5e-109;		
Matches 199;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRIEIPVLPNRVGLPINORFTL	60	
Db	1	MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRIEIPVLPNRVGLPINORFTL	60	
QY	61	VELSNHAELSVTLALDVTVNAVYVGYRAGNSAYFFHPDQEDAEATHLFTDQNYRTFAF	120	
Db	61	VELSNHAELSVTLALDVTVNAVYVGYRAGNSAYFFHPDQEDAEATHLFTDQNYRTFAF	120	
QY	121	GNVDRLEQAGNLEINELGNGLPELEAISALYYSTGTQTLPTLARSFIICQMISEAA	180	
Db	121	GNVDRLEQAGNLEINELGNGLPELEAISALYYSTGTQTLPTLARSFIICQMISEAA	180	
QY	181	RFQYIEGEMRTIRYNRRS	199	

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Db 181 RFQIEGEMTRIRYNRS 199
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RESULT 2
US-10-083-336A-10
; Sequence 10, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083.336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-10
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Best Local Similarity 100.0%; Pred. No. 1.5e-109; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;
Qy 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRAEAIHTLFTDVQNRYPFAG 60
Db 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRAEAIHTLFTDVQNRYPFAG 60
Qy 61 VELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNOEDAEAIHTLFTDVQNRYPFAG 120
Db 61 VELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNOEDAEAIHTLFTDVQNRYPFAG 120
Qy 121 GNYDRLEQLAGNLRNIELGNGPLEEAI SALLYVYSTGGTOLPTLARSFFIICOMISEAA 180
Db 121 GNYDRLEQLAGNLRNIELGNGPLEEAI SALLYVYSTGGTOLPTLARSFFIICOMISEAA 180
Qy 181 RFQIEGEMTRIRYNRS 199
Db 181 RFQIEGEMTRIRYNRS 199
RESULT 3
US-10-083-336A-3
; Sequence 3, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083.336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-3
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Best Local Similarity 100.0%; Pred. No. 5.5e-109; Indels 0; Gaps 0;
Matches 198; Conservative 0; Mismatches 0;
Qy 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRAEAIHTLFTDVQNRYPFAG 61
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182 FOYIEGEMTRIRYNRS 199
181 FOYIEGEMTRIRYNRS 198
RESULT 4
US-10-127-890-1
; Sequence 1, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1
Query Match 99.5%; Score 1020; DB 12; Length 267;
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Best Local Similarity 100.0%; Pred. No. 8.5e-109; Mismatches 0; Indels 0; Gaps 0;
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DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 60

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QY 122 GNYDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAAR 181
DB 121 GNYDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAAR 180

QY 182 FOYIEGEMRTRIRYNRRS 199
DB 181 FOYIEGEMRTRIRYNRRS 198

RESULT 5
US-10-083-336A-1
; Sequence 1, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-1

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Best Local Similarity 100.0%; Pred. No. 2.6e-108;
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DB 156 GNYDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAAR 215

QY 182 FOYIEGEMRTRIRYNRRS 199
DB 216 FOYIEGEMRTRIRYNRRS 233

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US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)

; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-7

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Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 62

QY 64 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 123
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 122

QY 124 YDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAARFQ 183
DB 123 YDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAARFQ 182

QY 184 YIEGEMRTRIRYNRRS 199
DB 183 YIEGEMRTRIRYNRRS 198

RESULT 7
US-10-282-935-1
; Sequence 1, Application US/10282935
; Publication No. US20030143193A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; FILE REFERENCE: US/10/282,935
; CURRENT APPLICATION NUMBER: US/10/282,935
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/125,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-282-935-1

Query Match 98.5%; Score 1010; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-107;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 63
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 62

QY 64 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 123
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 122

QY 124 YDRLEQLAGNLRNIELGNGLPLEEASALYYSTGGTQGLPTLARSFFIICIQMISEAARFQ 183

Db 123 YDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAAAPQ 182
QY 184 YIEGEMTRIRYNRRS 199
Db 183 YIEGEMTRIRYNRRS 198

RESULT 8

US-10-440-796-1
; Sequence 1, Application US/10440796
; Publication No. US20040009148A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETTIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROKANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
; TITLE OF INVENTION: SYNDROME (VLS)
; FILE REFERENCE: UTSD:603
; CURRENT APPLICATION NUMBER: US/10/440,796
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-440-796-1

Query Match 98.5%; Score 1010; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-107; Indels 0; Gaps 0;
Matches 196; Conservative 0; Mismatches 0;
QY 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 63
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 62
QY 64 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAFGN 123
Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAFGN 122
QY 124 YDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAAAPQ 183
Db 123 YDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAAAPQ 182
QY 184 YIEGEMTRIRYNRRS 199
Db 183 YIEGEMTRIRYNRRS 198

RESULT 9

US-10-083-336A-6
; Sequence 6, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-6

Query Match 93.3%; Score 956; DB 12; Length 189;
Best Local Similarity 95.0%; Pred. No. 1.2e-101; Indels 10; Gaps 1;
Matches 189; Conservative 0; Mismatches 0;
QY 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFIL 60
Db 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFIL 50
QY 61 VELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAF 120
Db 51 VELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAF 110
QY 121 GGNVDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAA 180
Db 111 GGNVDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAA 170
QY 181 RFQYIEGEMTRIRYNRRS 199
Db 171 RFQYIEGEMTRIRYNRRS 189

RESULT 10

US-10-083-336A-11
; Sequence 11, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-11

Query Match 93.3%; Score 956; DB 12; Length 190;
Best Local Similarity 95.0%; Pred. No. 1.2e-101; Indels 10; Gaps 1;
Matches 189; Conservative 0; Mismatches 0;
QY 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFIL 60
Db 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFIL 50
QY 61 VELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAF 120
Db 51 VELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAF 110
QY 121 GGNVDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAA 180
Db 111 GGNVDRLEQAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFIIQMISEAA 170
QY 181 RFQYIEGEMTRIRYNRRS 199
Db 171 RFQYIEGEMTRIRYNRRS 189

RESULT 11

US-10-083-336A-4
; Sequence 4, Application US/10083336A
; Publication No. US20030181665A1

GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-4

Query Match 92.8%; Score 951; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 4.5e-101;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVHEIPVLPNRVGLPINQRFILV 61
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILV 50

QY 62 ELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
Db 51 ELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 110

QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFIIQMISEAAAR 181
Db 111 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFIIQMISEAAAR 170

QY 182 FQYIEGEMTRIRYNRRS 199
Db 171 FQYIEGEMTRIRYNRRS 188

RESULT 12
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match 91.8%; Score 941; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 6.3e-100;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVHEIPVLPNRVGLPINQRFILV 63
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILV 52

QY 64 SNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 123
Db 53 SNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 112

QY 124 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFIIQMISEAAARFQ 183

Db 113 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFIIQMISEAAARFQ 172

QY 184 YIEGEMTRIRYNRRS 199
Db 173 YIEGEMTRIRYNRRS 188

RESULT 13
US-10-083-336A-9
; Sequence 9, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-9

Query Match 91.2%; Score 934.5; DB 12; Length 185;
Best Local Similarity 93.4%; Pred. No. 3.5e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVHEIPVLPNRVGLPINQRFILV 61
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47

QY 62 ELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
Db 48 ELSNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 107

QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFIIQMISEAAAR 181
Db 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTARSFIIQMISEAAAR 167

QY 182 FQYIEGEMTRIRYNRRS 199
Db 168 FQYIEGEMTRIRYNRRS 185

RESULT 14
US-10-083-336A-2
; Sequence 2, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-2

Query Match 73.0%; Score 748; DB 12; Length 179;
Best Local Similarity 100.0%; Pred. No. 9.4e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINQRFILV 60
QY 51 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQNRYYTFAFG 110
Db 61 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQNRYYTFAFG 120
QY 111 GNYDRLEQLAGNLRNIEIENGNGPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 170
Db 121 GNYDRLEQLAGNLRNIEIENGNGPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 180
QY 171 FOYIEGEMTRIRYNRRS 188
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 2

US-08-338-793D-61
; Sequence 61, Application US/08338793D
; Patent No. 5840521
; GENERAL INFORMATION:
; APPLICANT: Barth, Peter Thomas
; TITLE OF INVENTION: VECTOR
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY CUSHMAN
; ADDRESSEE: INTELLECTUAL PROPERTY GROUP OF
; ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM PC/XT/AT Compatibles
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft word or ASCII editors
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,793D
; FILING DATE: 08-No. 5840521-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842,081
; FILING DATE: 26-Feb-92
; CLASSIFICATION: 435
; APPLICATION NUMBER: 9104017.0
; FILING DATE: 26-Feb-91
; APPLICATION NUMBER: 9109188.4
; FILING DATE: 29-Apr-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokullis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: DJB/9901/215431/TGM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-338-793D-61

Query Match 98.4%; Score 950; DB 2; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.2e-102;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINQRFILV 50
Db 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINQRFILV 60

QY 51 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQNRYYTFAFG 110
Db 61 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQNRYYTFAFG 120
QY 111 GNYDRLEQLAGNLRNIEIENGNGPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 170
Db 121 GNYDRLEQLAGNLRNIEIENGNGPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 180
QY 171 FOYIEGEMTRIRYNRRS 188
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 3

US-09-538-873-1
; Sequence 1, Application US/09538873
; Patent No. 6566500
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETTIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
; FILE REFERENCE: UTSD:603
; CURRENT APPLICATION NUMBER: US/09/538,873
; CURRENT FILING DATE: 2000-03-30
; EARLIER APPLICATION NUMBER: 60/126,826
; EARLIER FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-538-873-1

Query Match 98.4%; Score 950; DB 4; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.2e-102;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINQRFILV 50
Db 1 MYPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINQRFILV 60
QY 51 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQNRYYTFAFG 110
Db 61 ELSNHAELS VTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQNRYYTFAFG 120
QY 111 GNYDRLEQLAGNLRNIEIENGNGPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 170
Db 121 GNYDRLEQLAGNLRNIEIENGNGPLEEASALYYSTGGTQPLTARSFFIICQMISEAAR 180
QY 171 FOYIEGEMTRIRYNRRS 188
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 4

US-07-901-707-1
; Sequence 1, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhardt, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve F.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; Composition and Use for Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-1

Query Match 97.5%; Score 941; DB 1; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
Qy 3 PKQPIINFTTAGATVQSYTNFIRAVGRGLT-----VLPNRVGLPINQRFILVEL 52
Db 3 PKQPIINFTTAGATVQSYTNFIRAVGRGLTGADVRHEIPVLPNRVGLPINQRFILVEL 62
Qy 53 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVYTFAGGN 112
Db 63 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVYTFAGGN 122
Qy 113 YDRLEQLAGNLRNIELNGPLBEAISALYYSTGGTQPLTARSFIIICIMISEAARFQ 172
Db 123 YDRLEQLAGNLRNIELNGPLBEAISALYYSTGGTQPLTARSFIIICIMISEAARFQ 182
Qy 173 YIEGEMTRIRYNRRS 188
Db 183 YIEGEMTRIRYNRRS 198

RESULT 5
US-07-988-430-1
Sequence 1, Application US/07988430
Patent No. 5416202
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-988-430-1

Query Match 97.5%; Score 941; DB 1; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
Qy 3 PKQPIINFTTAGATVQSYTNFIRAVGRGLT-----VLPNRVGLPINQRFILVEL 52
Db 3 PKQPIINFTTAGATVQSYTNFIRAVGRGLTGADVRHEIPVLPNRVGLPINQRFILVEL 62
Qy 53 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVYTFAGGN 112
Db 63 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRVYTFAGGN 122
Qy 113 YDRLEQLAGNLRNIELNGPLBEAISALYYSTGGTQPLTARSFIIICIMISEAARFQ 172
Db 123 YDRLEQLAGNLRNIELNGPLBEAISALYYSTGGTQPLTARSFIIICIMISEAARFQ 182
Qy 173 YIEGEMTRIRYNRRS 188
Db 183 YIEGEMTRIRYNRRS 198

RESULT 6
US-08-425-336-1
Sequence 1, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-1

Query Match 97.5%; Score 941; DB 1; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFATTAGATVQSYNFIKAVRGRLT-----VLPNRVGLPINORFILVEL 52
Db 3 PKQYPIINFATTAGATVQSYNFIKAVRGRLTGVDRHEIPVLPNRVGLPINORFILVEL 62
QY 53 SNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDQVQRYTFAFGN 112
Db 63 SNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDQVQRYTFAFGN 122
QY 113 YDRLEQAGNLRNIEIUNGPLEEASALYYSTGGTQPLTARSFIIQIMISEARFQ 172
Db 123 YDRLEQAGNLRNIEIUNGPLEEASALYYSTGGTQPLTARSFIIQIMISEARFQ 182
QY 173 YIEGEMRTRIRYNRRS 188
Db 183 YIEGEMRTRIRYNRRS 198

RESULT 7
US-08-488-113B-1
Sequence 1, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-1
Query Match 97.5%; Score 941; DB 1; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKQYPIINFATTAGATVQSYNFIKAVRGRLT-----VLPNRVGLPINORFILVEL 52
Db 3 PKQYPIINFATTAGATVQSYNFIKAVRGRLTGVDRHEIPVLPNRVGLPINORFILVEL 62
QY 53 SNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDQVQRYTFAFGN 112
Db 63 SNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDQVQRYTFAFGN 122
QY 113 YDRLEQAGNLRNIEIUNGPLEEASALYYSTGGTQPLTARSFIIQIMISEARFQ 172
Db 123 YDRLEQAGNLRNIEIUNGPLEEASALYYSTGGTQPLTARSFIIQIMISEARFQ 182
QY 173 YIEGEMRTRIRYNRRS 188
Db 183 YIEGEMRTRIRYNRRS 198
RESULT 8
US-08-477-484B-1
Sequence 1, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/477,484B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 267 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-477-484B-1

Query Match 97.5%; Score 941; DB 1; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 KQKPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 52
DB 3 KQKPIINFTTAGATVQSYTNFIRAVRGLTADVRHEIPVLPNRVGLPINQRFILVEL 62
QY 53 SNHAELSVTLALDVNNAVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGN 112
DB 53 SNHAELSVTLALDVNNAVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGN 122
QY 113 YDRLEQLAGNLRENIELNGPLSEASALYYSTGGTQPLTARSFFIICIMISEARFQ 172
DB 123 YDRLEQLAGNLRENIELNGPLSEASALYYSTGGTQPLTARSFFIICIMISEARFQ 182
QY 173 YIEGEMTRIRYNRRS 188
DB 183 YIEGEMTRIRYNRRS 198

RESULT 9
US-08-646-360-1

;; Sequence 1, Application US/08646360
;; Patent No. 5837491
;; GENERAL INFORMATION:
;; APPLICANT: Better, Marc D.
;; APPLICANT: Carroll, Stephen F.
;; APPLICANT: Studnika, Gary M.
;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70.P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 267 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-646-360-1
Query Match 97.5%; Score 941; DB 2; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
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DB 3 KQKPIINFTTAGATVQSYTNFIRAVRGLTADVRHEIPVLPNRVGLPINQRFILVEL 62
QY 53 SNHAELSVTLALDVNNAVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGN 112
DB 53 SNHAELSVTLALDVNNAVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAFGN 122
QY 113 YDRLEQLAGNLRENIELNGPLSEASALYYSTGGTQPLTARSFFIICIMISEARFQ 172
DB 123 YDRLEQLAGNLRENIELNGPLSEASALYYSTGGTQPLTARSFFIICIMISEARFQ 182
QY 173 YIEGEMTRIRYNRRS 188

Db 183 YIEGEMTRIRYNRS 198
113 YDRLEQLAGNLRENIEIENGNGPLEEASALYYSTGGTQLTPLARSFIQIMISEARFQ 172
123 YDRLEQLAGNLRENIEIENGNGPLEEASALYYSTGGTQLTPLARSFIQIMISEARFQ 182
173 YIEGEMTRIRYNRS 188
183 YIEGEMTRIRYNRS 198
RESULT 11
US-09-136-389-1
; Sequence 1, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-765-1
Query Match 97.5%; Score 941; DB 3; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
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Db 3 PKQYPIINFTAGATVQSYTNFIRAVRGLTGTGADVVRHEIPVLENRVGLPINQRFILVEL 62
Qy 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDDEAETHLFTDQVQRYTFAPGN 112
Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDDEAETHLFTDQVQRYTFAPGN 122

QY 3 PKOYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
Db 3 PKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 62
QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 112
Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 122
QY 113 YDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIICQMISEAARFQ 172
Db 123 YDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIICQMISEAARFQ 182
QY 173 YIEGEMRTRIRYNRRS 188
Db 183 YIEGEMRTRIRYNRRS 198
RESULT 12
US-09-610-838-1
; Sequence 1, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-610-838-1
Query Match 97.5%; Score 941; DB 4; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
QY 3 PKOYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
Db 3 PKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 62
QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 112
Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVYTFAGGN 122
QY 113 YDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIICQMISEAARFQ 172
Db 123 YDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIICQMISEAARFQ 182
QY 173 YIEGEMRTRIRYNRRS 188
Db 183 YIEGEMRTRIRYNRRS 198
RESULT 13
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhardt, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Bicknell,
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-09487-1

Query Match          97.5%; Score 941; DB 5; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
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QY 113 YDRLEQAGNLRNLELNGPLSEASALYYSTGGTOLPTLARSFFICIMISEAARFQ 172
Db 123 YDRLEQAGNLRNLELNGPLSEASALYYSTGGTOLPTLARSFFICIMISEAARFQ 182
QY 173 YIEGEMTRIRYNRRS 188
Db 183 YIEGEMTRIRYNRRS 198

RESULT 14
US-08-356-786-8
; Sequence 8, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-8
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Query Match          97.5%; Score 941; DB 2; Length 268;
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
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QY 53 SNHAELSVTLALDVNTAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQVNRYYTFAFGN 112
Db 64 SNHAELSVTLALDVNTAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQVNRYYTFAFGN 123
QY 113 YDRLEQAGNLRNLELNGPLSEASALYYSTGGTOLPTLARSFFICIMISEAARFQ 172
Db 124 YDRLEQAGNLRNLELNGPLSEASALYYSTGGTOLPTLARSFFICIMISEAARFQ 183
QY 173 YIEGEMTRIRYNRRS 188
Db 184 YIEGEMTRIRYNRRS 199

RESULT 15
US-08-378-761A-27
; Sequence 27, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-27

Query Match          97.5%; Score 941; DB 1; Length 290;
Best Local Similarity 94.9%; Pred. No. 1.5e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
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QY 53 SNHAELSVTLALDVTNAVYVGYRAGNSAYFFHPDNOEDAEATHLFTDVQNEYTFAGGN 112
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 113 YDRLEQLAGNLRNIELGNGLPEEAISALYYYSTGGTQPTLARSFIIICIMISEAARFQ 172
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 147 YDRLEQLAGNLRNIELGNGLPEEAISALYYYSTGGTQPTLARSFIIICIMISEAARFQ 206
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 173 YIEGEMRTRIRYNRES 188
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 207 YIEGEMRTRIRYNRES 222
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Job time : 10.8703 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 24.2491 Seconds
(without alignments)
1623.314 Million cell updates/sec

Title: US-10-083-336A-8

Perfect score: 965

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Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 20938283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	965	100.0	188	12	US-10-083-336A-8
2	956	99.1	188	12	US-10-083-336A-4
3	956	99.1	189	12	US-10-083-336A-6
4	956	99.1	190	12	US-10-083-336A-11
5	950	98.4	198	12	US-10-083-336A-7
6	950	98.4	267	12	US-10-282-935-1
7	950	98.4	267	12	US-10-440-796-1
8	941	97.5	198	12	US-10-083-336A-3
9	941	97.5	199	12	US-10-083-336A-5
10	941	97.5	200	12	US-10-083-336A-10
11	941	97.5	267	12	US-10-127-890-1
12	941	97.5	576	12	US-10-083-336A-1
13	923.5	96.3	185	12	US-10-083-336A-9
14	669	69.3	179	12	US-10-083-336A-2
15	336	34.8	247	10	US-09-792-793A-39

16	336	34.8	247	12	US-10-127-890-6	Sequence 6, Appli
17	336	34.8	247	12	US-10-375-209A-39	Sequence 39, Appli
18	336	34.8	289	12	US-10-280-679B-4	Sequence 4, Appli
19	305	31.6	247	10	US-09-792-793A-34	Sequence 34, Appli
20	305	31.6	247	12	US-10-375-209A-34	Sequence 34, Appli
21	297.5	30.8	251	12	US-10-282-935-3	Sequence 3, Appli
22	297.5	30.8	251	12	US-10-440-796-3	Sequence 3, Appli
23	273	28.3	263	12	US-10-127-890-7	Sequence 7, Appli
24	272	28.2	263	12	US-10-127-890-4	Sequence 4, Appli
25	257.5	26.7	248	12	US-10-127-890-5	Sequence 5, Appli
26	254	26.3	252	9	US-09-347-064-2	Sequence 2, Appli
27	254	26.3	252	9	US-09-347-064-8	Sequence 8, Appli
28	245.5	25.4	251	12	US-10-127-890-107	Sequence 107, App
29	244.5	25.3	251	12	US-10-127-890-106	Sequence 106, App
30	244.5	25.3	251	12	US-10-127-890-110	Sequence 110, App
31	244.5	25.3	251	12	US-10-127-890-111	Sequence 111, App
32	243.5	25.2	251	9	US-09-765-527-247	Sequence 247, App
33	243.5	25.2	251	12	US-10-127-890-2	Sequence 2, Appli
34	243.5	25.2	251	12	US-10-127-890-99	Sequence 99, Appli
35	243.5	25.2	251	12	US-10-127-890-100	Sequence 100, App
36	243.5	25.2	251	12	US-10-127-890-101	Sequence 101, App
37	243.5	25.2	251	12	US-10-127-890-102	Sequence 102, App
38	243.5	25.2	251	12	US-10-127-890-103	Sequence 103, App
39	243.5	25.2	251	12	US-10-127-890-104	Sequence 104, App
40	243.5	25.2	251	12	US-10-127-890-105	Sequence 105, App
41	243.5	25.2	316	12	US-10-074-596-1	Sequence 1, Appli
42	243.5	25.2	507	12	US-10-074-596-11	Sequence 11, Appli
43	242.5	25.1	251	12	US-10-127-890-109	Sequence 109, App
44	242.5	25.1	293	9	US-09-765-527-259	Sequence 259, App
45	242.5	25.1	309	9	US-09-765-527-253	Sequence 253, App

ALIGNMENTS

RESULT 1

US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match	100.0%;	Score	965;	DB	12;	Length	188;
Best Local Similarity	100.0%;	Pred. NO.	1.1e-102;				
Matches	188;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MVPKQYPIINFTTAGATVQS	YTFIRAVRGRLTVLPNVRGLPINQRFILVLSNHAELSV	60			
Db	1	MVPKQYPIINFTTAGATVQS	YTFIRAVRGRLTVLPNVRGLPINQRFILVLSNHAELSV	60			
Qy	61	TALDVTNAYVGVGRAGNSAYFFHPDQEDAEATHLFTDVQNYRTTFAFGNYDRLEQLA	120				
Db	61	TALDVTNAYVGVGRAGNSAYFFHPDQEDAEATHLFTDVQNYRTTFAFGNYDRLEQLA	120				
Qy	121	GNLRENTLGNPLEEAEISALYYSTGCTQLPTLARSFIICIQMISEARFQYIEGEMRT	180				
Db	121	GNLRENTLGNPLEEAEISALYYSTGCTQLPTLARSFIICIQMISEARFQYIEGEMRT	180				
Qy	181	RIRYNRS	188				

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Db      181 RYNNRS 188
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RESULT 2
US-10-083-336A-4
; Sequence 4, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-4

Query Match      99.1%; Score 956; DB 12; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAEISVTL 62
Db      3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAEISVTL 62
QY      63 ALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFPGGNYDRLEQLAGN 122
Db      63 ALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFPGGNYDRLEQLAGN 122
QY      123 LRENIELGNGPLEEASALYYSTGTQPTLARSFIIICIQMISEAARFOYIEGEMRTRI 182
Db      123 LRENIELGNGPLEEASALYYSTGTQPTLARSFIIICIQMISEAARFOYIEGEMRTRI 182
QY      183 RYNNRS 188
Db      183 RYNNRS 188
|||||
RESULT 3
US-10-083-336A-6
; Sequence 6, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-6

Query Match      99.1%; Score 956; DB 12; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAEISVTL 62
Db      3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAEISVTL 62
QY      63 ALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFPGGNYDRLEQLAGN 122
Db      63 ALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFPGGNYDRLEQLAGN 122
QY      123 LRENIELGNGPLEEASALYYSTGTQPTLARSFIIICIQMISEAARFOYIEGEMRTRI 182
Db      123 LRENIELGNGPLEEASALYYSTGTQPTLARSFIIICIQMISEAARFOYIEGEMRTRI 182
QY      183 RYNNRS 188
Db      183 RYNNRS 188
|||||
RESULT 4
US-10-083-336A-11
; Sequence 11, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-11

Query Match      99.1%; Score 956; DB 12; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAEISVTL 62
Db      3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAEISVTL 62
QY      63 ALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFPGGNYDRLEQLAGN 122
Db      63 ALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFPGGNYDRLEQLAGN 122
QY      123 LRENIELGNGPLEEASALYYSTGTQPTLARSFIIICIQMISEAARFOYIEGEMRTRI 182
Db      123 LRENIELGNGPLEEASALYYSTGTQPTLARSFIIICIQMISEAARFOYIEGEMRTRI 182
QY      183 RYNNRS 188
Db      183 RYNNRS 188
|||||
RESULT 5
US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

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Db      4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAEISVTL 63
QY      63 ALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFPGGNYDRLEQLAGN 122
Db      64 ALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFPGGNYDRLEQLAGN 123
QY      123 LRENIELGNGPLEEASALYYSTGTQPTLARSFIIICIQMISEAARFOYIEGEMRTRI 182
Db      124 LRENIELGNGPLEEASALYYSTGTQPTLARSFIIICIQMISEAARFOYIEGEMRTRI 183
QY      183 RYNNRS 188
Db      184 RYNNRS 189
|||||
RESULT 4
US-10-083-336A-11
; Sequence 11, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-11

Query Match      99.1%; Score 956; DB 12; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAEISVTL 62
Db      4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAEISVTL 63
QY      63 ALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFPGGNYDRLEQLAGN 122
Db      64 ALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTAFPGGNYDRLEQLAGN 123
QY      123 LRENIELGNGPLEEASALYYSTGTQPTLARSFIIICIQMISEAARFOYIEGEMRTRI 182
Db      124 LRENIELGNGPLEEASALYYSTGTQPTLARSFIIICIQMISEAARFOYIEGEMRTRI 183
QY      183 RYNNRS 188
Db      184 RYNNRS 189
|||||
RESULT 5
US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

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; LENGTH: 198
 ; TYPE: PRT
 ; ORGANISM: Ricinus communis
 US-10-083-336A-7

Query Match 98.4%; Score 950; DB 12; Length 198;
 Best Local Similarity 94.9%; Pred. No. 6.4e-101;
 Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 1 MYPKQYPIINFITAGATVQSYTNFIRAVGRILT-----VLPNRVGLPINORFILV 50
 Db 1 MYPKQYPIINFITAGATVQSYTNFIRAVGRILT-----VLPNRVGLPINORFILV 60
 QY 51 ELSNHAELSVTALDVTNAYVGVYRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 110
 Db 61 ELSNHAELSVTALDVTNAYVGVYRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 120
 QY 111 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAAR 170
 Db 121 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAAR 180
 QY 171 FOYIEGEMTRIRYNRS 188
 Db 181 FOYIEGEMTRIRYNRS 198

RESULT 6

US-10-282-935-1

; Sequence 1, Application US/10282935
 ; Publication No. US20030143193A1

GENERAL INFORMATION:

APPLICANT: VITETTA, ELLEN S.

APPLICANT: GHETIE, VICTOR F.

APPLICANT: SMALLSHAW, JOAN

APPLICANT: BALUNA, ROXANA G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF

FILE REFERENCE: US/884US

CURRENT APPLICATION NUMBER: US/10/282,935

CURRENT FILING DATE: 2002-10-29

PRIOR APPLICATION NUMBER: 09/538,873

PRIOR FILING DATE: 2000-03-30

PRIOR APPLICATION NUMBER: 60/126,826

PRIOR FILING DATE: 1999-03-30

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 1

LENGTH: 267

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-10-282-935-1

Query Match

Best Local Similarity 98.4%; Score 950; DB 12; Length 267;

Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 1 MYPKQYPIINFITAGATVQSYTNFIRAVGRILT-----VLPNRVGLPINORFILV 50
 Db 1 MYPKQYPIINFITAGATVQSYTNFIRAVGRILT-----VLPNRVGLPINORFILV 60
 QY 51 ELSNHAELSVTALDVTNAYVGVYRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 110
 Db 61 ELSNHAELSVTALDVTNAYVGVYRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 120
 QY 111 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAAR 170
 Db 121 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAAR 180
 QY 171 FOYIEGEMTRIRYNRS 188
 Db 181 FOYIEGEMTRIRYNRS 198

Db 181 FOYIEGEMTRIRYNRS 198

RESULT 7

US-10-440-796-1

; Sequence 1, Application US/10440796
 ; Publication No. US20040009148A1

GENERAL INFORMATION:

APPLICANT: VITETTA, ELLEN S.

APPLICANT: GHETIE, VICTOR F.

APPLICANT: SMALLSHAW, JOAN

APPLICANT: BALUNA, ROXANA G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK

FILE REFERENCE: US/603

CURRENT APPLICATION NUMBER: US/10/440,796

CURRENT FILING DATE: 2003-05-19

PRIOR APPLICATION NUMBER: US/09/538,873

PRIOR FILING DATE: 2000-03-30

PRIOR APPLICATION NUMBER: 60/126,826

PRIOR FILING DATE: 1999-03-30

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 1

LENGTH: 267

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-10-440-796-1

Query Match 98.4%; Score 950; DB 12; Length 267;

Best Local Similarity 94.9%; Pred. No. 9.8e-101;

Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 1 MYPKQYPIINFITAGATVQSYTNFIRAVGRILT-----VLPNRVGLPINORFILV 50
 Db 1 MYPKQYPIINFITAGATVQSYTNFIRAVGRILT-----VLPNRVGLPINORFILV 60
 QY 51 ELSNHAELSVTALDVTNAYVGVYRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 110
 Db 61 ELSNHAELSVTALDVTNAYVGVYRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 120
 QY 111 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAAR 170
 Db 121 GNYDRLEQLAGNLENIELGNGLPLEEALSALYYSTGGTQLPTLARSFIIQIMISEAAR 180
 QY 171 FOYIEGEMTRIRYNRS 188
 Db 181 FOYIEGEMTRIRYNRS 198

RESULT 8

US-10-083-336A-3

Sequence 3, Application US/10083336A

Publication No. US20030181665A1

GENERAL INFORMATION:

APPLICANT: Olson, Mark A

APPLICANT: Millard, Charles B

APPLICANT: Byrnes, Michael P

APPLICANT: Wannemacher, Robert W

TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof

FILE REFERENCE: P67452US0 (RIID 01-58)

CURRENT APPLICATION NUMBER: US/10/083,336A

CURRENT FILING DATE: 2002-05-21

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 3

LENGTH: 198

TYPE: PRT

ORGANISM: Ricinus communis

US-10-083-336A-3

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; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-10

Query Match          97.5%; Score 941; DB 12; Length 198;
Best Local Similarity 94.9%; Pred. No. 7e-100;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNRVGLPINQRFILVEL 62

QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFGN 112
Db 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFGN 122

QY 113 YDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIIQIMISEAARFQ 172
Db 123 YDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIIQIMISEAARFQ 182

QY 173 YIEGEMRTRIRYNRRS 188
Db 183 YIEGEMRTRIRYNRRS 198

RESULT 9
US-10-083-336A-5
; Sequence 5, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-5

Query Match          97.5%; Score 941; DB 12; Length 199;
Best Local Similarity 94.9%; Pred. No. 7e-100;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
Db 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNRVGLPINQRFILVEL 63

QY 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFGN 112
Db 64 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFGN 123

QY 113 YDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIIQIMISEAARFQ 172
Db 124 YDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQTLPTLARSFIIQIMISEAARFQ 183

QY 173 YIEGEMRTRIRYNRRS 188
Db 184 YIEGEMRTRIRYNRRS 198

RESULT 10
US-10-083-336A-10
; Sequence 10, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W

```

ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-127-890-1

Query Match 97.5%; Score 941; DB 12; Length 267;
 Best Local Similarity 94.9%; Pred. No. 1.1e-99;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVREIPLVLPNRVGLPINQRFILVEL 62

QY 53 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGGN 112
 DB 63 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGGN 122

QY 113 YDRLEQLAGNLRNIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQ 172
 DB 123 YDRLEQLAGNLRNIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQ 182

QY 173 YIEGEMTRIRYNRRS 188
 DB 183 YIEGEMTRIRYNRRS 198

RESULT 12
 US-10-083-336A-1
 ; Sequence 1, Application US/10083336A
 ; Publication No. US20030181665A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olson, Mark A
 ; APPLICANT: Millard, Charles B
 ; APPLICANT: Byrne, Michael P
 ; APPLICANT: Wannemacher, Robert W
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
 ; FILE REFERENCE: P67452US0 (RIID 01-58)
 ; CURRENT APPLICATION NUMBER: US/10/083,336A
 ; CURRENT FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 576
 ; TYPE: PRT
 ; ORGANISM: Ricinus communis
 US-10-083-336A-1

Query Match 97.5%; Score 941; DB 12; Length 576;
 Best Local Similarity 94.9%; Pred. No. 3.2e-99;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVREIPLVLPNRVGLPINQRFILVEL 97

QY 53 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGGN 112
 DB 98 SNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGGN 157

QY 113 YDRLEQLAGNLRNIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQ 172
 DB 123 YDRLEQLAGNLRNIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQ 182

Db 158 YDRLEQLAGNLRNIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQ 217
 QY 173 YIEGEMTRIRYNRRS 188
 DB 218 YIEGEMTRIRYNRRS 233

RESULT 13
 US-10-083-336A-9
 ; Sequence 9, Application US/10083336A
 ; Publication No. US20030181665A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olson, Mark A
 ; APPLICANT: Millard, Charles B
 ; APPLICANT: Byrne, Michael P
 ; APPLICANT: Wannemacher, Robert W
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
 ; FILE REFERENCE: P67452US0 (RIID 01-58)
 ; CURRENT APPLICATION NUMBER: US/10/083,336A
 ; CURRENT FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Ricinus communis
 US-10-083-336A-9

Query Match 96.3%; Score 929.5; DB 12; Length 185;
 Best Local Similarity 98.4%; Pred. No. 1.3e-98;
 Matches 183; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAELSVTL 62
 DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVELSNHAELSVTL 59

QY 63 ALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGGNYDRLEQLAGN 122
 DB 60 ALDVTNAVVGVRAGNSAYFFHPDQEDAEATHLFTDQVQRYTFAGGNYDRLEQLAGN 119

QY 123 LRENIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQYIEGEMTRI 182
 DB 120 LRENIELNGNGPLEAISALYYSTGGTQPLTLARSFFIICQMISEAARFQYIEGEMTRI 179

QY 183 RYNRRS 188
 DB 180 RYNRRS 185

RESULT 14
 US-10-083-336A-2
 ; Sequence 2, Application US/10083336A
 ; Publication No. US20030181665A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olson, Mark A
 ; APPLICANT: Millard, Charles B
 ; APPLICANT: Byrne, Michael P
 ; APPLICANT: Wannemacher, Robert W
 ; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
 ; FILE REFERENCE: P67452US0 (RIID 01-58)
 ; CURRENT APPLICATION NUMBER: US/10/083,336A
 ; CURRENT FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 179
 ; TYPE: PRT
 ; ORGANISM: Ricinus communis
 US-10-083-336A-2

Query Match 69.3%; Score 669; DB 12; Length 179;
 Best Local Similarity 93.0%; Pred. No. 1.1e-68;
 Matches 132; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

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QY      3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINORFILVEL 52
Db      38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVERHEIPVLPNRVGLPINORFILVEL 97
QY     53 SNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDVQNRVTFPAFGGN 112
Db     98 SNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDVQNRVTFPAFGGN 157
QY    113 YDRLEQLAGNLRNIELNGNPL 134
Db    158 YDRLEQLAGNLRNIELNGNPL 179
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RESULT 15

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US-09-792-793A-39
; Sequence 39, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Trichosantheus kirilowii
US-09-792-793A-39
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Query Match      34.8%; Score 336; DB 10; Length 247;
Best Local Similarity 38.9%; Pred. No. 3.6e-30;
Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;
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QY      9 INFTTAGATVQSYTNFIRAVRGRLTLPN-----RVGLPINORFILVELSNHAEL 58
Db     2 VSFELSGATSSSYGVFISNR---KALFNERKLYDIPLLRSSLPGSQRYALIHITNYADE 58
QY     59 SVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRVTFPAFGGNYDRLE 117
Db     59 TISVAIDVTNVIIMGYRAGDTSYFF--NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ 115
QY    118 QLAGNLRNIELNGNPLEEAI SAIYVYSTGQTQPLARSFIICIMISEAARFQYIEGE 177
Db    116 TAAGKIRENIPGLPALDLSAITLTFYNAN-----SAASALMVLIOSTSEARYKFEQQ 170
QY    178 MRTRI 182
Db    171 IGKEV 175
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Search completed: February 10, 2004, 16:53:54
Job time : 25.2491 secs
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:35 ; Search time 10.1735 Seconds
(without alignments)
1777.145 Million cell updates/sec

Title: US-10-083-336A-8
Perfect score: 965
Sequence: 1 MWPQYPIINFTAGATVQS.....ARFOYIEGMRTIRYNRS 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	94.1	97.5	576	1 RLCSA	ricin D precursor
2	851.5	88.2	564	1 RLCSAG	agglutinin precursor
3	336	34.8	289	1 RLTSZ	rRNA N-glycosidase
4	327.5	33.9	528	2 S2431	abrin-d precursor
5	327.5	33.9	562	2 S16022	abrin-c precursor
6	326	33.8	247	2 JU0393	karasurin - Mongol
7	326	33.8	247	2 JU0393	karasurin-B - Tric
8	326	33.8	289	2 JU0393	karasurin C - Tric
9	323	33.5	527	2 S32430	abrin-b precursor
10	310.5	32.2	251	2 S39761	abrin (clone 7.2)
11	303.5	31.5	528	1 T2LSA	abrin-a precursor
12	300.5	31.1	278	2 S23519	beta-luffin - smoo
13	293.5	30.4	250	2 JU0108	luffin-b - smooch
14	274.5	28.4	277	2 S22494	rRNA N-glycosidase
15	274	28.4	286	2 S25560	rRNA N-glycosidase
16	273	28.3	286	1 RLPUGG	rRNA N-glycosidase
17	273	28.3	570	2 S62627	agglutinin I precu
18	270	28.0	245	2 JU0480	rRNA N-glycosidase
19	267	27.7	286	2 JU0435	rRNA N-glycosidase
20	264	27.4	254	2 PU0018	mistletoe lectin I
21	243.5	25.2	316	2 JU0753	rRNA N-glycosidase
22	186.5	19.3	294	2 S28421	rRNA N-glycosidase
23	174	18.0	278	2 A39817	rRNA N-glycosidase
24	170	17.6	313	2 S17757	rRNA N-glycosidase
25	168.5	17.5	261	2 JU0401	antiviral protein
26	148.5	15.4	289	2 T12573	rRNA N-glycosidase
27	138	14.3	272	2 JU4811	betavulgin - beet
28	131	13.6	253	2 S28542	rRNA N-glycosidase
29	127	13.2	253	2 S28539	rRNA N-glycosidase

ALIGNMENTS

RESULT 1

RLCSA
ricin D precursor - castor bean
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C>Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text change 16-Jul-1999
C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041; MUID:86067214; PMID:2999712
A:Accession: A24041
A:Molecule type: DNA
A:Residues: 1-576 <HAL>
A:Cross-references: GB:X03179; NID:g21083; PIDN:CAA26939.1; PID:g21083
R:Tregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 1992
A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
A:Reference number: S20513; MUID:92163016; PMID:1371405
A:Accession: S20513
A:Molecule type: DNA
A:Residues: 1-576 <TRE>
A:Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085
R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Eur. J. Biochem. 148, 265-270, 1985
A:Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A:Reference number: A24614; MUID:85179479; PMID:3838723
A:Accession: A24614
A:Molecule type: mRNA
A:Residues: 12-75, 'D', 77-550, 'R', 552-576 <LAM>
A:Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078
R:Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
A:Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile Cha
A:Reference number: A03372
A:Accession: A03372
A:Molecule type: protein
A:Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>
A:Note: this paper cites the others in the series providing experimental details for the
R:Araki, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan
A:Reference number: A24010
A:Accession: A24010
A:Molecule type: protein
A:Residues: 315-383, 'PS', 386-576 <ARA>
R:Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A:Title: Primary structure of Ala chain of ricin D.
A:Reference number: A03374
A:Accession: A03374
A:Molecule type: protein

30 127 13.2 253 2 S29931 rRNA N-glycosidase
31 124 12.8 283 2 S05205 rRNA N-glycosidase
32 123 12.7 253 2 S28541 rRNA N-glycosidase
33 122 12.6 310 2 S46239 ribosome-inactivat
34 121 12.5 292 1 RLQHG2 rRNA N-glycosidase
35 116.5 12.1 293 2 S17519 rRNA N-glycosidase
36 116 12.0 275 2 S33631 tritin - wheat
37 115 11.9 253 2 A58923 rRNA N-glycosidase
38 114 11.8 280 1 ALBH rRNA N-glycosidase
39 112 11.6 280 2 JC5848 protein synthesis
40 110 11.4 236 2 S17932 rRNA N-glycosidase
41 109 11.3 319 2 S21940 hypothetical prote
42 108 11.2 319 2 I54695 shiga-like toxin I
43 108 11.2 319 2 E90779 shiga toxin 2 subu
44 108 11.2 319 2 G85640 shiga toxin 2 subu
45 107.5 11.1 318 2 S01032 Shiga-like toxin I

A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',405-427,'E',529-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>
 A;Note: This paper, one of a series, summarizes the experimental details for the determination of the complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
 R;Ready, M.P.; Kim, Y.; Robertus, J.D.
 Proteins 10, 270-278, 1991
 A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of action.
 A;Reference number: A48237; MUID:91352006; PMID:1881883
 A;Contents: annotation: active site
 R;Robertus, J.D.
 Proteins 10, 260-269, 1991
 A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
 A;Reference number: A48238; MUID:91352005; PMID:1881882
 A;Contents: annotation: X-ray crystallography, 2.5 angstroms
 R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.
 Proteins 10, 251-259, 1991
 A;Title: Structure of ricin A-chain at 2.5 angstroms.
 A;Reference number: A48239; MUID:91352004; PMID:1881881
 A;Contents: annotation: X-ray crystallography, 2.5 angstroms
 C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which inactivates the 60S ribosomal subunit. The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subunit. The B chain is also responsible for cell agglutination (lectin).
 C;Comment: This protein is cytotoxic and very poisonous to animals.
 C;Superfamily: ricin; rRNA N-glycosidase homology
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
 F;1-35/Domain: signal sequence #status predicted <SIG>
 F;36-302/Product: ricin D chain A #status experimental <ACH>
 F;36-293/Domain: rRNA N-glycosidase homology <RNG>
 F;315-576/Product: ricin D chain B #status experimental <BCH>
 F;331-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats
 F;45-409,449/Binding site: carboxylate (Asn) (covalent) #status experimental
 F;115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F;212/Active site: Glu #status experimental
 F;215/Active site: Arg #status predicted
 F;294-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental
 F;336,349,360/Binding site: N-acetylglucosamine (Asp, Gln, Asn) #status experimental
 F;548,569/Binding site: N-acetylglucosamine (Asp, Asn) #status experimental
 Query Match 97.5%; Score 941; DB 1; Length 576;
 Best Local Similarity 94.9%; Pred. No. 1.8e-76;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 3 PKQYPIINFAGTAGVQSYNFIKAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 38 PKQYPIINFAGTAGVQSYNFIKAVRGRLT-----VLPNRVGLPINQRFILVEL 97
 QY 53 SNHAEISVTLALDVNAYVYVGRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPGNN 112
 DB 98 SNHAEISVTLALDVNAYVYVGRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPGNN 157
 QY 113 YDRLEQLAGNLRENIELNGPFLPEEAISALYYSTGGTQPLTARSFIIQIMISEARFQ 172
 DB 158 YDRLEQLAGNLRENIELNGPFLPEEAISALYYSTGGTQPLTARSFIIQIMISEARFQ 217
 QY 173 YIEGEMTRIRYNRRS 188
 DB 218 YIEGEMTRIRYNRRS 233
 RESULT 2
 RLCSAG
 agglutinin precursor - castor bean
 N;Contents: rRNA N-glycosidase (EC 3.2.2.22)
 C;Species: Ricinus communis (castor bean)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C;Accession: A24261; A24210
 R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
 J. Biol. Chem. 260, 15682-15686, 1985
 A;Title: The primary structure of Ricinus communis agglutinin. Comparison with ricin.
 A;Reference number: A24261; MUID:86059449; PMID:2999130
 A;Accession: A24261
 A;Molecule type: mRNA
 A;Residues: 1-564 <ROB>
 A;Cross-references: GB:M12089; NID:G169700; PIDN:AAA33869.1; PID:G169701

R;Araki, T.; Yoshioka, Y.; Funatsu, G.
 Biochim. Biophys. Acta 872, 277-285, 1986
 A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
 A;Reference number: A24210
 A;Accession: A24210
 A;Molecule type: protein
 A;Residues: 303-325,'F',327-330,'T',332-361,'D',363-373,'G',375-403,'T',405-551,'V',553-559,'E',561-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>
 C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared with ricin.
 C;Superfamily: ricin; rRNA N-glycosidase homology
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-290/Product: agglutinin chain A #status predicted <ACH>
 F;35-281/Domain: rRNA N-glycosidase homology <RNG>
 F;303-564/Product: agglutinin chain B #status experimental <BCH>
 F;319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats
 F;34,259/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F;200,203/Active site: Glu, Arg #status predicted
 F;282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
 F;324,337,348/Binding site: N-acetylglucosamine (Asp, Gln, Asn) #status predicted
 F;397,437/Binding site: carboxylate (Asn) (covalent) #status experimental
 F;536,557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 Query Match 88.2%; Score 851.5; DB 1; Length 564;
 Best Local Similarity 86.7%; Pred. No. 2.9e-70;
 Matches 170; Conservative 7; Mismatches 8; Indels 11; Gaps 2;
 QY 3 PKQYPIINFAGTAGVQSYNFIKAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 27 PKQYPIINFAGTAGVQSYNFIKAVRGRLT-----VLPNRVGLPINQRFILVEL 86
 QY 53 SNHAEISVTLALDVNAYVYVGRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPGNN 112
 DB 87 SNHAEISVTLALDVNAYVYVGRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPGNN 146
 QY 113 YDRLEQLAGNLRENIELNGPFLPEEAISALYYSTGGTQPLTARSFIIQIMISEARFQ 172
 DB 147 YDRLEQLAGNLRENIELNGPFLPEEAISALYYSTGGTQPLTARSFIIQIMISEARFQ 205
 QY 173 YIEGEMTRIRYNRRS 188
 DB 206 YIEGEMTRIRYNRRS 221
 RESULT 3
 RLRTZT
 rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian snake
 N;Alternate names: alpha-TCS; type I ribosome-inactivating protein
 C;Species: Trichosanthin kirilowii (Mongolian snake-gourd)
 C;Date: 30-Sep-1988 #sequence_revision 26-Jan-1996 #text_change 23-Mar-2001
 C;Accession: JT0566; A36274; JC1093; A36273; JT0003
 R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.X.; Ng, T.B.; Yeung, H.W.
 Gene 97, 267-272, 1991
 A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.
 A;Reference number: JT0566; MUID:91153657; PMID:1999291
 A;Accession: JT0566
 A;Molecule type: mRNA
 A;Residues: 1-289 <SHA>
 A;Cross-references: GB:M34858; NID:G170536; PIDN:AAA34207.1; PID:G170537
 R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
 J. Biol. Chem. 265, 8670-8674, 1990
 A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribosome-inactivating protein.
 A;Reference number: A36274; MUID:90256790; PMID:2341400
 A;Accession: A36274
 A;Molecule type: DNA
 A;Residues: 1-233,'T',235-246,'M',248-289 <CHO>
 A;Cross-references: GB:J05434; NID:G170534; PIDN:AAA34206.1; PID:G170535
 R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
 Acta Genet. Sin. 21, 42-51, 1994
 A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
 A;Reference number: JC1093; MUID:94271613; PMID:8009348
 A;Accession: JC1093

A:Molecule type: DNA
 A:Residues: 1-72, 'V' 74-90, 'S' 92-233, 'T' 235-267, 'D' 269-289 <ZHE>
 A:Cross-references: GB:S70176; NID:9547148; PID:AA831048.1; PID:9547149
 R:Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
 J. Biol. Chem. 265, 8665-8669, 1990
 A:Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for ab
 A:Reference number: A36273; MUID:90256789; PMID:2341399
 A:Accession: A36273
 A:Molecule type: protein
 A:Residues: 24-270 <COL>
 R:Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
 Pure Appl. Chem. 58, 789-798, 1986
 A:Title: Scientific evaluation of Tian Hua Fen (THEF): history, chemistry and application
 A:Reference number: JT0003
 A:Accession: JT0003
 A:Molecule type: protein
 A:Residues: 24-56, 'L' 58-59, 'I' 61-71, 'I' 73-81, 85-86, 'L' 88-92, 'DAGLPRNAV' 93-142, 'GL'
 A:Experimental source: tuber
 R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
 submitted to the Brookhaven Protein Data Bank, July 1994
 A:Reference number: A67091; PDB:1MRJ
 A:Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-
 R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
 submitted to the Brookhaven Protein Data Bank, July 1994
 A:Reference number: A67092; PDB:1MRK
 A:Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24
 R:Xiong, J.P.; Xia, Z.X.; Wang, Y.
 submitted to the Brookhaven Protein Data Bank, December 1994
 A:Reference number: A66711; PDB:1TCS
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
 R:Xiong, J.P.; Xia, Z.X.; Wang, Y.
 Nat. Struct. Biol. 1, 695-700, 1994
 A:Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re
 A:Reference number: A58622; MUID:95360714; PMID:7634073
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms
 C:Comment: Alpha-trichosanthin has been used to induce abortions.
 C:Genetics:
 A:Gene: tcs
 C:Function:
 A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA thez
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 C:Keywords: abortifacient; glycosidase; hydrolase; root; toxin
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-270/Product: trichosanthin alpha #status experimental <MAT>
 F:27-266/Domain: rRNA N-glycosidase homology <RNG>
 F:271-289/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F:93,183,186/Active site: Tyr, Glu, Arg #status predicted

Query Match 34.8%; Score 336; DB 1; Length 289;
 Best Local Similarity 38.9%; Pred. No. 2.6e-23;
 Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;

Qy 9 INFETAGATVQSYTNFIRAVRGRITVLPN-----RVGLPINQRFILVELSNHAE 58
 Db 25 VSFRLSGATSSYGVFISNLR---KALPNERKLYDIPILRSLSPLGSGQRYALIHLYTNVADE 81

Qy 59 SVTLALDVTNAYVVGVRAGNSAYFFHPDQDAEALTHLFTDQVQNYTFAGGNYDRL 117
 Db 82 TISVAIDVTNVIYNGVRAGDSYFF---NEASATEAKYVFDAMRKVTLPSYNGYERLQ 138

Qy 118 QLAGNLRENIELNGPLEEALISALYYSTGGTQPLTLARSFFICQMISEAARFQYIEG 177
 Db 139 TAAGKIRENIPGLPALDSAITLTFYNNAN-----SAASALMWLIQSTSEAAKYKFFIEQQ 193

Qy 178 MRTRI 182
 Db 194 IGKRV 198

RESULT 4
 S32431
 A:Cross-references: EMBL:X55667; NID:g16084; PID:CAA39202.1; PID:g16085
 N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
 A:Title: Precursor - Indian licorice (fragment)
 C:Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating

C:Species: Abrus precatorius (Indian licorice)
 C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
 C:Accession: S32431; S34408
 R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
 J. Mol. Biol. 229, 263-267, 1993
 A:Title: Primary structure of three distinct isoabirins determined by cDNA sequencing. Cor
 A:Reference number: S32429; MUID:95132798; PMID:8421313
 A:Accession: S32431
 A:Molecule type: mRNA
 A:Residues: 1-528 <HUN>
 A:Cross-references: GB:M98346
 R:Hung, C.; Lee, M.; Lee, T.; Lin, J.
 submitted to the EMBL Data Library, March 1993
 A:Reference number: S34408
 A:Accession: S34408
 A:Molecule type: mRNA
 A:Residues: 1-169, 'C' 171-320, 'L' 322-528 <HU2>
 A:Cross-references: GB:M98346
 C:Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating
 The A and B chains are linked by a single disulfide bond, which is essential for toxicit
 C:Superfamily: ricin; rRNA N-glycosidase homology
 C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p)
 F:1-251/Product: abrin-d chain A #status predicted <ACH>
 F:7-246/Domain: rRNA N-glycosidase homology <RNG>
 F:261-528/Product: abrin-d chain B #status predicted <BOH>
 F:283-325, 326-366, 369-407, 414-449, 453-492, 495-528/Region: 40-residue repeats
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:164,167/Active site: Glu, Arg #status predicted
 F:200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:247-269, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
 F:288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
 F:500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 33.9%; Score 327.5; DB 2; Length 528;
 Best Local Similarity 43.9%; Pred. No. 3.3e-22;
 Matches 82; Conservative 22; Mismatches 68; Indels 15; Gaps 4;

Qy 5 QYPIINFETAGATVQSYTNFIRAVRGRIT-----VLPNRVGLPINQRFILVELSNHA 56
 Db 1 ODQVIRKFTTEGATSSQYKQFIEALRQLTGGLIHDPVLPDPTTVEERNEYITVELSNSE 60

Qy 57 ELSVTALDVTNAYVVGVRAGNSAYFFHPDQDAEALTHLFTDQVQNYTFAGGNYDRL 116
 Db 61 RESIEVGIDVTNAYVAVRAGSOSYFL---RDPASASTYLFPGTQ-RYSIRFDGSGDL 116

Qy 117 EQLAGNLRENIELNGPLEEALISALYYSTGGTQPLTLARSFFICQMISEAARFQYIEG 176
 Db 117 ERWAHQTRREISLGLQALTHAIS---FLRSGASNDSEKANTLIVIQMASEAARYISN 173

Qy 177 EMRTIR 183
 Db 174 RVGVSR 180

RESULT 5
 S16022
 A:Title: Precursor - Indian licorice
 N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Abrus precatorius (Indian licorice)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
 C:Accession: S16022
 R:Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M.
 Eur. J. Biochem. 198, 723-732, 1991
 A:Title: Preproabrin: genomic cloning, characterisation and the expression of the A-chain
 A:Reference number: S16022; MUID:91266957; PMID:2050149
 A:Accession: S16022
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-562 <WOO>
 A:Cross-references: EMBL:X55667; NID:g16084; PID:CAA39202.1; PID:g16085
 C:Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating
 The A and B chains are linked by a single disulfide bond, which is essential for toxicit

Query Match	33.8%;	Score 326;	DB 2;	Length 247;
Best Local Similarity	39.6%;	Pred. No. 1.7e-22;		
Matches	72;	Conservative 44;	Mismatches 50;	Indels 16; Gaps 5;
QY	9	INFTTAGATVQSYTNFIRAVR-----GRLTVP-NEVGLPIINORFTLVLSNHAELSVT	61	
Db	2	VSEFLSGATSSSYGVFISNRKALPYERKLYDIPLLRSTIPGSGRYALIHITNVADETIS	61	
QY	62	LALDVTNAYVYVGRAGNSAYFFHPDQEDA-EAITHLFTDVQNYRTFAFGNYDRLEOLA	120	
Db	62	VAIDVTNVYVMYGRAGDTSYFF--NEASATEAAKYVFKDKRKVTLPYSGNYERLQIAA	118	
QY	121	GNLRENIELNGPLPEEASIALYXYSTGGTQLPTLARSFICIQIMSEAAFPVTEGEMPT	180	
Db	119	GKIRENIPLGLPALDSAITTLFYNN-----SAASALMVIQSTSEARYKFIEQQIGK	173	
QY	181	RI	182	
Db	174	RV	175	

A;Molecule type: DNA
A;Residues: 1-289 <MIZ>
A;Cross-references: DDBJ:AB000666; NID:g2329830; PIDN:BAA21786.1; PID:g2329831
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
A;Reference number: JCS032; MUID:97108848; PMID:8951169
A;Accession: JCS033
A;Status: preliminary
A;Molecule type: protein
A;Residues: 22-270 <KON>
C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti
C;Superfamily: rRNA N-glycosidase
F;22-270/Product: karasurin C #status predicted <MAC>
F;24-270/Product: karasurin A #status predicted <MAA>
F;27-266/Domain: rRNA N-glycosidase homology <RNG>

Query Match 33.8%; Score 326; DB 2; Length 289;
Best Local Similarity 39.6%; Pred.No.2.1e-22;
Matches 72; Conservative 44; Mismatches 50; Indels 16; Gaps 5;

Db 173 RVGVSIRTN 181

RESULT 10

C39761

abrin (clone 7.2) precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C>Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: C39761; S14471
R:Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A:Title: Direct molecular cloning and expression of two distinct abrin A-chains
A:Reference number: A39761; MUID:91201329; PMID:2016300
A:Accession: C39761
A:Molecule type: DNA
A:Residues: 'M', 1-251 <EV2>
R:Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A:Description: Direct molecular cloning of two distinct abrin A-chains.
A:Reference number: S14471
A:Accession: S14471
A:Molecule type: DNA
A:Residues: 'M', 1-251 <EV2>
A:CROSS-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C:Superfamily: ricin; rRNA N-glycosidase homology
K:Keywords: duplication; glycosidase; hydrolase; lectin; toxin
F:1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F:7-246/Domain: rRNA N-glycosidase homology <RNG>
F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:164,167/Active site: Glu, Arg #status predicted

Query Match 32.2%; Score 310.5; DB 2; Length 251;
Best Local Similarity 43.2%; Pred. No. 4.7e-21;
Matches 79; Conservative 22; Mismatches 67; Indels 15; Gaps 4;

Qy 9 INPTTAGATVQSNTNFRAVRGRL-----TVLPNRVGLPINFILVELSNHAELSV 60
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
5 IKFTSGATSSQSYKQTEALRELRGLTHDIPVLDRPTVEERNRYITVELSNSERESI 64

Qy 61 TLALDTNVAVVGYRAGNSAYFFHPDNQDEAAITHLFIDVQNVRTFAFGNYDLRQLA 120
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
65 EVGIDVTNAVVAIRAGSSQYFL--RDAPASASTYLTGTQ-RYSLRFDGSYGDLERWA 120

Qy 121 GNLRNIHELGNGLPEAIISALYYISTGGTQPLTLARSFTICIMISEARFOYIEGMET 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
121 HQPREQISLGLOALTHAIS--FLRSASNDKEAKRTLIVIIQMASEARARYINSRVGV 177

Qy 181 RIR 183
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
178 SIR 180

RESULT 11

TZLSA

abrin-a precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C>Date: 31-Dec-1993 #sequence_revision 01-Aug-1997 #text change 16-Jul-1999
C:Accession: S32429; JTF0202; A39761; JC1398; S14472; S24133; S74110; S74111
R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A:Title: Primary structure of three distinct isoabirins determined by cDNA sequen
A:Reference number: S32429; MUID:93132798; PMID:8421313
A:Accession: S32429
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'E', 2-528 <HUN>
A:CROSS-references: GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295
A>Note: the coding region for the sequence shown is preceded by an ATG codon
A>Note: residues 1-8 were derived from the synthesized primer
R:Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988

Query Match 30.4%; Score 293.5; DB 2; Length 250;

Search completed: February 10, 2004, 16:28:02
Job time : 10.1735 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:55 ; Search time 6.27131 Seconds
(without alignments)
1409.756 Million cell updates/sec

Title: US-10-083-336A-8

Perfect score: 965

Sequence: 1 MVPKQYPIINFITAGATVQS.....ARFQYIEGEMRTIRYNRS 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	941	97.5	576	1 RICI_RICCO	P02879 ricinus com
2	851.5	88.2	564	1 AGSL_RICCO	P06750 ricinus com
3	336	34.8	289	1 R1PT_TRIKI	P09989 trichosanthe
4	327.5	33.9	562	1 ABRG_ABRER	P28590 abrus prec
5	326	33.8	289	1 R1PS_TRIKI	P24478 trichosanthe
6	323	33.5	527	1 ABRB_ABRER	Q06077 abrus prec
7	320.5	33.2	282	1 R1P2_BRYDI	P98184 bryonia dio
8	307.5	31.9	563	1 N1GB_SAMNI	P33183 sambucus ni
9	305	31.6	290	1 R1P1_BRYDI	P33185 bryonia dio
10	303.5	31.5	528	1 ABRG_ABRER	P11140 abrus prec
11	293.5	30.4	250	1 R1P1_LUFVCY	P22851 luffa cylin
12	281.5	29.2	286	1 R1P1_CUCFI	Q9FRX4 cucumis fig
13	274.5	28.4	277	1 R1P1_LUFVCY	Q00465 luffa cylin
14	274	28.4	286	1 R1P2_MOMBA	P29339 momordica b
15	273	28.3	286	1 R1P1_MOMCH	P16094 momordica c
16	264	27.4	254	1 M1A_VISAL	P81446 viscum albu
17	257	26.6	294	1 R1P1_TRIAN	P56626 trichosanthe
18	243.5	25.2	316	1 R1P1_GELMU	P33186 gelonium mu
19	186.5	19.3	294	1 R1P1_PHYAM	Q33464 phytolacca
20	174	18.0	278	1 R1P1_MIRTA	P21326 mirabilis j
21	170	17.6	313	1 R1P1_PHYAM	P10297 phytolacca
22	168.5	17.5	261	1 R1P5_PHYAM	P23339 phytolacca
23	131	13.6	253	1 R1P7_SAPOF	Q41391 saponaria o
24	127	13.2	253	1 R1P5_SAPOF	Q41389 saponaria o
25	124	12.8	299	1 R1P6_SAPOF	P20656 saponaria o
26	122	12.6	310	1 R1P2_PHYAM	Q40772 phytolacca
27	121	12.5	292	1 R1P2_SAPOF	P27559 saponaria o
28	116.5	12.1	293	1 R1P0_D1ACA	P24476 dianthus ca
29	114	11.8	280	1 R1P2_HORVU	P04399 hordeum vul
30	110	11.4	236	1 R1P3_SAPOF	P27560 saponaria o
31	107	11.2	319	1 S1TA_BP933	P09385 bacterioph
32	107	11.1	280	1 R1P1_HORVU	P22244 hordeum vul
33	101	10.5	300	1 R1P3_MAIZE	P25891 zea mays (m

RESULT 1				
R1CI_	RICCO	STANDARD;	PRT;	576 AA.
ID	R1CI_RICCO			
AC	P02879; P02880;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ricin precursor [Contains: Ricin A chain (rRNA N-glycosidase)			
DE	(EC 3.2.2.22); Ricin B chain]			
OS	Ricinus communis (Castor bean)			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosidia I; Malpighiales; Euphorbiaceae; Ricinus.			
OX	NCBI_TaxID=3398;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067214; PubMed=2999712;			
RA	Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,			
RA	Weaver R.F.;			
RT	"Genomic cloning and characterization of a ricin gene from Ricinus			
RT	communis.";			
RL	Nucleic Acids Res. 13:8019-8033 (1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92163016; PubMed=1371405;			
RA	Tregear J.W., Roberts L.M.;			
RT	"The lectin gene family of Ricinus communis: cloning of a functional			
RT	ricin gene and three lectin pseudogenes.";			
RL	Plant Mol. Biol. 18:515-525 (1992).			
RN	[3]			
RP	SEQUENCE OF 12-576 FROM N.A.			
RX	MEDLINE=85179479; PubMed=3838723;			
RA	Lamb A., Roberts L.M., Lord J.M.;			
RT	"Nucleotide sequence of cloned cDNA coding for preproricin.";			
RL	Eur. J. Biochem. 148:265-270 (1985).			
RN	[4]			
RP	SEQUENCE OF 36-302.			
RA	Yoshitake S., Funatsu G., Funatsu M.;			
RT	"Isolation and sequences of peptic peptides, and the complete			
RT	sequence of Ile chain of ricin-D.";			
RL	Agric. Biol. Chem. 42:1267-1274 (1978).			
RN	[5]			
RP	SEQUENCE OF 315-576.			
RA	Funatsu G., Kimura M., Funatsu M.;			
RT	"Primary structure of Ala chain of ricin D.";			
RL	Agric. Biol. Chem. 43:2221-2224 (1979).			
RN	[6]			
RP	CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.			
RX	MEDLINE=90344223; PubMed=1368517;			
RA	Kimura Y., Kusuku H., Tada M., Takagi S., Funatsu G.;			
RT	"Structural analyses of sugar chains from ricin A-chain variant.";			
RL	Agric. Biol. Chem. 54:157-162 (1990).			
RN	[7]			
RP	REVIEW.			
RX	MEDLINE=21480122; PubMed=11595634;			
RA	Olsnes S., Kozlov J.V.;			

P28522 zea mays (m
P08026 bacterioph
P25892 zea mays (m
P10149 bacterioph
O67411 aquifex aco
P75255 mycoplasma
Q00531 hordeum vul
Q90xb4 homo sapien
P27561 saponaria o
Q00971 vibrio prot
P44755 haemophilus

ALIGNMENTS

RT "Ricin."; CC
 RL Toxicon 39:1723-1728(2001). CC
 RN [8] CC
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS). CC
 RX MEDLINE=87165983; PubMed=3558397; CC
 RA Monfort W., Villafranca J.E., Monzingo A.F., Ernst S.R., Katzin B., CC
 RUTENBER E., XUONG N.H., HAMLIN R., ROBERTUS J.D.; CC
 RT "The three-dimensional structure of ricin at 2.8 A."; CC
 RL J. Biol. Chem. 262:5398-5403(1987). CC
 RN [9] CC
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. CC
 RX MEDLINE=91352004; PubMed=1881881; CC
 RA Katzin B.J., Collins E.J., Robertus J.D.; CC
 RT "Structure of ricin A-chain at 2.5 A."; CC
 RL Proteins 10:251-259(1991). CC
 RN [10] CC
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN. CC
 RX MEDLINE=91352005; PubMed=1881882; CC
 RA RUTENBER E., ROBERTUS J.D.; CC
 RT "Structure of ricin B-chain at 2.5-A resolution."; CC
 RL Proteins 10:260-269(1991). CC
 RN [11] CC
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN. CC
 RX MEDLINE=95082010; PubMed=7990130; CC
 RA WESTON S.A., TUCKER A.D., THATCHER D.R., DERBYSHIRE D.J., CC
 RA PAUPIT R.A.; CC
 RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution."; CC
 RL J. Mol. Biol. 244:410-422(1994). CC
 RN [12] CC
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215. CC
 RX MEDLINE=96374222; PubMed=8780513; CC
 RA DAY P.J., ERNST S.R., FRANKEL A.E., MONZINGO A.F., PASCAL J.M., CC
 RA MOLINA-SVINTH M.C., ROBERTUS J.D.; CC
 RT "Structure and activity of an active site substitution of ricin A CC
 chain."; CC
 RL Biochemistry 35:11098-11103(1996). CC
 RN [13] CC
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. CC
 RX MEDLINE=97240820; PubMed=9086280; CC
 RA YAN X., HOLLIS T., SVINTH M., DAY P., MONZINGO A.F., MILNE G.W., CC
 RA ROBERTUS J.D.; CC
 RT "Structure-based identification of a ricin inhibitor."; CC
 RL J. Mol. Biol. 266:1043-1049(1997). CC
 RN [14] CC
 RP MUTAGENESIS. CC
 RX MEDLINE=93165632; PubMed=1287657; CC
 RA KIN Y., ROBERTUS J.D.; CC
 RT "Analysis of several key active site residues of ricin A chain by CC
 mutagenesis and x-ray crystallography."; CC
 RL Protein Eng. 5:775-779(1992). CC
 CC -|- FUNCTION: Ricin is highly toxic to animal cells and to a less CC
 CC extent to plant cells. The A chain is responsible for inhibiting CC
 CC protein synthesis through the catalytic inactivation of 60S CC
 CC ribosomal subunits. It acts as a glycosidase that removes a CC
 CC specific adenine residue from an exposed loop of 28S ribosomal CC
 CC RNA. As this loop is involved in the binding of elongation CC
 CC factors, the modified ribosomes are unable to support protein CC
 CC synthesis. The A chain can inactivate a few thousand ribosomes CC
 CC per minute, thus inactivating them faster than the cell can make CC
 CC new ones. A single A-chain molecule can therefore kill an animal CC
 CC cell. The B chain binds to cell receptors and facilitates the CC
 CC entry into the cell of the A chain; B chains are also responsible CC
 CC for cell agglutination (lectin activity). It binds to beta-D- CC
 CC galactopyranoside moieties. CC
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one CC
 CC specific adenosine on the 28S rRNA. CC
 CC -|- SUBUNIT: Disulfide-linked dimer of A and B chains. CC
 CC -|- DOMAIN: The B chain is composed of two domains, each domain CC
 CC consists of 3 homologous subdomains (alpha, beta, gamma). CC
 CC -|- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE CC
 CC MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271. CC
 CC -|- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME- CC
 CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY. CC

CC -|- SIMILARITY: Contains 2 ricin B-type lectin domains. CC
 CC -|- CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS CC
 CC WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3). CC
 CC -|- DATABASE: NAME=Protein Spotlight; CC
 CC NOTE=Issue 31 of February 2003; CC
 CC WWW="http://www.expasy.org/spotlight/articles/sptlc031.html". CC
 CC ----- CC
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 CC ----- CC
 CC EMBL; X03179; CAA36939.1; -; CC
 CC EMBL; X52908; CAA37095.1; -; CC
 CC EMBL; X02388; CAA26230.1; -; CC
 CC EMBL; A12892; CAA01058.1; -; CC
 CC PIR; A24041; RUCSD. CC
 CC PDB; 2AA1; 31-JAN-94. CC
 CC PDB; 1APG; 31-JAN-94. CC
 CC PDB; 1FMP; 31-OCT-93. CC
 CC PDB; 1IFS; 14-JAN-98. CC
 CC PDB; 1IFT; 14-JAN-98. CC
 CC PDB; 1IFU; 14-JAN-98. CC
 CC PDB; 1RUC; 31-OCT-93. CC
 CC PDB; 1OBS; 16-JUN-97. CC
 CC PDB; 1OBT; 16-JUN-97. CC
 CC PDB; 1BR5; 02-SEP-98. CC
 CC PDB; 1BR6; 02-SEP-98. CC
 CC PDB; 1IL3; 16-JAN-02. CC
 CC PDB; 1IL4; 16-JAN-02. CC
 CC PDB; 1IL9; 16-JAN-02. CC
 CC GlycoSuiteDB; P02879; -; CC
 CC InterPro; IPR000772; Ricin_B_lectin. CC
 CC InterPro; IPR001574; RIP. CC
 CC Pfam; PF00652; Ricin_B_lectin; 6. CC
 CC Pfam; PF00161; RIP; 1. CC
 CC PRINTS; P000396; SHIGARICIN. CC
 CC SMART; SM00458; RICIN; 2. CC
 CC PROSITE; PS02311; RICIN_B_LECTIN; 2. CC
 CC PROSITE; PS00275; SHIGA_RICIN; 1. CC
 CC Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; CC
 CC Glycoprotein; Lectin; Signal; 3D-structure. CC
 CC SIGNAL 1 35 CC
 CC CHAIN 36 302 CC
 CC PEPTIDE 303 314 CC
 CC CHAIN 315 576 CC
 CC CHAIN 321 448 CC
 CC DOMAIN 451 575 CC
 CC REPEAT 331 373 CC
 CC REPEAT 374 414 CC
 CC REPEAT 417 449 CC
 CC REPEAT 462 497 CC
 CC REPEAT 501 540 CC
 CC REPEAT 543 570 CC
 CC ACT SITE 212 212 CC
 CC DISULFID 294 318 CC
 CC DISULFID 334 353 CC
 CC DISULFID 377 394 CC
 CC DISULFID 465 478 CC
 CC DISULFID 504 521 CC
 CC CARBOHYD 45 45 CC
 CC CARBOHYD 271 271 CC
 CC CARBOHYD 409 409 CC
 CC CARBOHYD 449 449 CC
 CC CARBOHYD 76 76 CC
 CC CONFLICT 551 551 CC
 CC CONFLICT 43 47 CC
 CC STRAND 49 50 CC
 CC TURN 49 50 CC
 CC N-LINKED (GLCNAC. . .). CC
 CC /FTIC-CAR 000080. CC
 CC N-LINKED (GLCNAC. . .) (IN MINOR FORM). CC
 CC /FTIC-CAR 000081. CC
 CC N-LINKED (GLCNAC. . .). CC
 CC N-LINKED (GLCNAC. . .). CC
 CC E -> D (IN REF. 3). CC
 CC A -> R (IN REF. 3). CC

Query Match 97.5%; Score 941; DB 1; Length 576;
 Best Local Similarity 94.9%; Pred. No. 1,5e-79;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVRRHEIPVLPNRVGLPINQRFILVEL 97

QY 53 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGCN 112
 DB 98 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGCN 157

QY 113 YDRLEQLAGNLRENIELGNGLPELEAISALYYSTGTQTLPTLARSFIIQMISEAAARFQ 172
 DB 158 YDRLEQLAGNLRENIELGNGLPELEAISALYYSTGTQTLPTLARSFIIQMISEAAARFQ 217

QY 173 YIEGEMTRIRYNRRS 188
 DB 218 YIEGEMTRIRYNRRS 233

RESULT 2
 AGGL_RICCO STANDARD; PRT; 564 AA.

ID AGGL_RICCO
 AC P06750;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain).
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucotyledons; Malpighiales; Euphorbiaceae; Ricinus.
 OX NCBI_TaxID=3986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86059449; PubMed=2999130;
 RA Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
 RT "The primary sequence of Ricinus communis agglutinin. Comparison with ricin";
 RL J. Biol. Chem. 260:15682-15686 (1985).
 RN [2]
 RP SEQUENCE OF 303-564.
 RC TISSUE=Seed;
 RA Araki T., Yoshioka Y., Funatsu G.;
 RT "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds.";
 RL Biochim. Biophys. Acta 872:277-285 (1986).
 RN [3]
 RP SEQUENCE OF 303-337.
 RX MEDLINE=80178723; PubMed=6768555;
 RA Lin T.-S., Li S.-L.;
 RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis.";
 RL Eur. J. Biochem. 105:453-459 (1980).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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 CC -----
 CC EMBL; M12089; AAA33869.1; -;
 CC EMBL; S40368; AAB22384.1; -;

DR PIR; A24261; RLCSAG.
 DR HSP; P02879; IER6.
 DR GlycoSuiteDB; P06750; -;
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS02331; RICIN_B_LECTIN; 2.
 DR PROSITE; PS0275; SHIGA RICIN; 1.
 DR Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; Lectin; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 290 AGGLUTININ A CHAIN.
 FT PROPEP 291 302 LINKER PEPTIDE.
 FT CHAIN 303 564 AGGLUTININ B CHAIN.
 FT DOMAIN 309 436 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 439 563 RICIN B-TYPE LECTIN 2.
 FT REPEAT 319 361 1-ALPHA.
 FT REPEAT 362 402 1-BETA.
 FT REPEAT 405 437 1-GAMMA.
 FT REPEAT 450 485 2-ALPHA.
 FT REPEAT 489 528 2-BETA.
 FT REPEAT 531 558 2-GAMMA.
 FT ACT SITE 200 200 BY SIMILARITY.
 FT DISULFID 282 306 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 322 341 BY SIMILARITY.
 FT DISULFID 365 382 BY SIMILARITY.
 FT DISULFID 453 466 BY SIMILARITY.
 FT DISULFID 492 509 BY SIMILARITY.
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. .).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. .).
 FT CONFLICT 331 331 F -> T (IN REF. 2).
 FT CONFLICT 362 362 N -> D (IN REF. 2).
 FT CONFLICT 374 374 R -> G (IN REF. 2).
 FT CONFLICT 404 404 R -> T (IN REF. 2).
 FT CONFLICT 552 552 F -> V (IN REF. 2).
 SQ SEQUENCE 564 AA; 62851 MW; D455F2A72F609759 CRC64;

Query Match 88.2%; Score 851.5; DB 1; Length 564;
 Best Local Similarity 86.7%; Pred. No. 2.8e-71;
 Matches 170; Conservative 7; Mismatches 8; Indels 11; Gaps 2;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
 DB 27 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVRRHEIPVLPNRVGLPINQRFILVEL 86

QY 53 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGCN 112
 DB 87 SNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGCN 146

QY 113 YDRLEQLAGNLRENIELGNGLPELEAISALYYSTGTQTLPTLARSFIIQMISEAAARFQ 172
 DB 147 YDRLEQLAGNLRENIELGNGLPELEAISALYYSTGTQTLPTLARSFIIQMISEAAARFQ 205

QY 173 YIEGEMTRIRYNRRS 188
 DB 206 YIEGEMTRIRYNRRS 221

RESULT 3
 RIPT_TRIKI STANDARD; PRT; 289 AA.

ID RIPT_TRIKI
 AC P09989;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribosome-inactivating protein alpha-trichosanthin precursor (rRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
 OS Trichosanthes kirilowii (Mongolian snake-gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Maximowicz;
 RX MEDLINE=91153657; PubMed=1999291;
 RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
 RT "Cloning of trichosanthin cDNA and its expression in *Escherichia*
 RL *coli*.";
 RL Gene 97:267-272(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Maximowicz; TISSUE=Leaf;
 RX MEDLINE=90256790; PubMed=2341400;
 RA Chow T., Feldman R.A., Lovett M., Piatak M.;
 RT "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
 RL type I ribosome-inactivating protein.";
 RL J. Biol. Chem. 265:8670-8674(1990).
 RN (3)
 RP SEQUENCE OF 24-270.
 RC STRAIN=Maximowicz; TISSUE=Tuberous root;
 RX MEDLINE=90256789; PubMed=2341399;
 RA Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
 RT Wu P., Hwang K., Piatak M.;
 RL "Primary amino acid sequence of alpha-trichosanthin and molecular
 RL models for abrin A-chain and alpha-trichosanthin.";
 RL J. Biol. Chem. 265:8665-8669(1990).
 RN (4)
 RP SEQUENCE OF 24-270.
 RC TISSUE=Tuberous root;
 RX MEDLINE=94344957; PubMed=8066085;
 RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
 RT "Structure of trichosanthin at 1.88-A resolution.";
 RL Proteins 19:4-13(1994).
 RN (6)
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=95344383; PubMed=7619070;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
 RT "Studies on crystal structures, active-centre geometry and
 RL depurinatin mechanism of two ribosome-inactivating proteins.";
 RL Biochem. J. 309:285-298(1995).
 CC -1- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
 CC CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
 CC INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M34858; AAA34207.1; --
 DR EMBL; J05434; AAA34206.1; --
 DR PIR; JT0566; RLTTZ.
 DR PDB; 1MRJ; 07-FEB-95.
 DR PDB; 1MRK; 07-FEB-95.
 DR PDB; 1TCS; 10-JUL-95.
 DR PDB; 1J4G; 28-JAN-03.

DR PDB; 1NLI; 21-JAN-03.
 DR PDB; 1QD2; 24-APR-00.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA RICIN; 1.
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
 KW Toxin; Signal; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 270
 FT FT
 FT PROPEP 271 289
 FT ACT SITE 183 183
 FT CONFLICT 57 60
 FT CONFLICT 82 84
 FT CONFLICT 87 87
 FT CONFLICT 92 92
 FT CONFLICT 143 144
 FT CONFLICT 196 196
 FT CONFLICT 215 216
 FT CONFLICT 231 231
 FT CONFLICT 234 234
 FT CONFLICT 246 266
 FT CONFLICT 247 247
 FT STRAND 25 28
 FT TURN 30 31
 FT HELIX 34 46
 FT TURN 47 47
 FT STRAND 50 54
 FT TURN 55 56
 FT STRAND 57 60
 FT HELIX 66 69
 FT STRAND 70 76
 FT TURN 78 79
 FT STRAND 82 88
 FT TURN 89 92
 FT STRAND 93 99
 FT TURN 100 101
 FT STRAND 102 105
 FT HELIX 109 114
 FT TURN 115 117
 FT TURN 120 121
 FT STRAND 124 127
 FT HELIX 134 141
 FT TURN 142 142
 FT HELIX 145 147
 FT STRAND 150 150
 FT HELIX 152 163
 FT TURN 164 165
 FT HELIX 167 180
 FT TURN 181 181
 FT HELIX 182 186
 FT STRAND 187 187
 FT HELIX 188 195
 FT TURN 196 196
 FT STRAND 202 202
 FT TURN 205 226
 FT HELIX 227 230
 FT STRAND 231 239
 FT TURN 241 242
 FT STRAND 245 250
 FT TURN 251 252
 FT HELIX 254 258
 FT TURN 259 259
 FT STRAND 260 260
 FT TURN 263 263
 FT TURN 266 268
 SQ SEQUENCE 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;
 MISSING IN MATURE PROTEIN.
 BY SIMILARITY.
 IPLL -> LPLI (IN REF. 4).
 MISSING (IN REF. 4).
 I -> L (IN REF. 4).
 V -> VDAGLRNAVLI (IN REF. 4).
 KI -> GL (IN REF. 4).
 K -> S (IN REF. 4).
 WS -> LWL (IN REF. 4).
 Q -> T (IN REF. 4).
 S -> T (IN REF. 2).
 MISSING (IN REF. 4).
 T -> M (IN REF. 2).

Query Match 34.8%; Score 336; DB 1; Length 289;
 Best Local Similarity 38.9%; Pred. No. 6.5e-24;
 Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;

Qy	9	INFTTAGTVOYNYNFIKAVGRGLVLEN-----RVGLPINQRFILVELSNAEEL	58
Dd	25	VSEFLSGATSSYGVFISNLR---KALPNERKLYDIPLLRSSLPQSQRVALIHLITNYADE	81
Qy	59	SVTIALDVNTAAVVGYRAGNSAYPHPNQEDA-EAITHLFTDVQNRYTFARGGYNDRLE	117
Dd	82	TISVAIDVTNYIIMGYRAGDTSYFF--NEASATEAKYVFVDAMRKVTLPSYGNYERLQ	138
Qy	118	QLAGLRNIELGNGPLPEATSAIYYVTGGTQLPTLARSPFICIQMISEARFOYIEGE	177
Dd	139	TAACKIRENIPLGLPALDSAITLTLYNNAN-----SAASALMVLIQTSEAAARYFIEQQ	193
Qy	178	MRTRI	182
Dd	194	IGKRV	198

RESULT 4

ABCD	ABRPR		
ID	ABRC ABRPR	STANDARD;	PRT; 562 AA.
AC	P28590;		
DT	01-DEC-1992	(Rel. 24, Created)	
DT	01-DEC-1992	(Rel. 24, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Abirin-c precursor	[Contains: Abirin-c A chain (rRNA N-glycosidase)	
DE	(EC 3.2.2.2); Abirin-c B chain].		
OS	Abirus precatorius	(Indian licorice) (Crab's eye).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid1 I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.		
OX	NCBI_TaxID=3816;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUB=Leaf;		
RX	MEDLINE=91266957; PubMed=2050149;		
RT	Wood K.A., Lord J.M., Wawrzynczak E.J., Piatak M.;		
RT	"Preabirin: genomic cloning, characterisation and the expression of		
RT	the A-chain in <i>Escherichia coli</i> ."		
RL	Eur. J. Biochem. 198;723-732(1991).		
CC	-1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN		
CC	SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL		
CC	SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. THE		
CC	B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE		
CC	BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one		
CC	specific adenosine on the 28S rRNA.		
CC	-1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.		
CC	-1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN		
CC	CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).		
CC	-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-		
CC	INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.		
CC	-1- SIMILARITY: Contains 2 ricin B-type lectin domains.		

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EMBL; X55667; CAA39202.1; -.
 DR DR PIR; S16022; S16022.
 DR DR HSP; P11140; IABR.
 DR DR InterPro; IPR000772; Ricin_B_lectin.
 DR DR InterPro; IPR001574; RIP.
 DR DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR DR Pfam; PF00161; RIP; 1.
 DR DR PRINTS; PR00396; SHIGARICIN.
 DR DR SMART; SM00458; RICIN; 2.
 DR DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR DR PROSITE; PS00275; SHIGA_RICIN; 1.
 DR DR Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KW

QW	Glycoprotein; Lectin; Signal; Pyrrolidone carboxylic acid.	1	34	
FT	CHAIN	35	285	BY SIMILARITY.
FT	PEPTIDE	286	295	ABRIN C A CHAIN (BY SIMILARITY).
FT	CHAIN	296	562	LINKER PEPTIDE (BY SIMILARITY).
FT	DOMAIN	307	434	ABRIN C B CHAIN (BY SIMILARITY).
FT	DOMAIN	437	561	RICIN B-TYPE LECTIN 1.
FT	REPEAT	317	359	RICIN B-TYPE LECTIN 2.
FT	REPEAT	360	400	1-ALPHA.
FT	REPEAT	403	435	1-BETA.
FT	REPEAT	448	483	1-GAMMA.
FT	REPEAT	487	526	2-ALPHA.
FT	REPEAT	529	562	2-GAMMA.
FT	ACT SITE	198	198	BY SIMILARITY.
FT	DISULFID	281	303	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	320	339	BY SIMILARITY.
FT	DISULFID	363	389	BY SIMILARITY.
FT	DISULFID	451	464	BY SIMILARITY.
FT	DISULFID	490	507	BY SIMILARITY.
FT	MOD_RES	35	35	PYRROLIDONE CARBOXYLIC ACID
FT	CARBOHYD	234	234	(BY SIMILARITY).
FT	CARBOHYD	395	395	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	435	435	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	435	435	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	562 AA;	62817 MW;	1FDOABC7D7BA6278 CRC64;
QY	Query Match	33.9%;	Score 327.5;	DB 1; Length 562;
QY	Best Local Similarity	43.9%;	Pred. No. 8.9e-23;	Indels 15; Gaps 4;
QY	Matches	82;	Conservative 22;	Mismatches 68;
QY	5 QYPIINFTAGATVQSYTNFIRAVGRGLT-----VLPNRVGLPINQRFILVELSNHA	56		
QY	35 QDQVIRFTTEGATSQSYKQFIEALRQLTGLIHDIPVLDPDPTTVERNRYITVELSNSE	94		
QY	57 ELSVTALDVTNAYVGVYRAGNSAYFPHDPNQEDAEATHLFTDQNRXYTFAFGNYDRL	116		
QY	95 RESIEVGIDVTNAYVAYRAGSOSYFL---RDAPASASTVLPFGTQ-RYSLRFDGSYGDL	150		
QY	117 EQLAGNLRENIELNGPLBEAIALYVYSTGGTQLPTLARSFTICOMISEARFOYIEG	176		
QY	151 ERWAHQTRIEISLGLQALTHAIS---FLRSGASNDDEKARTLIVITOMASEAARYIISN	207		
QY	177 EMRETRIR	183		
QY	208 RVGVSIR	214		
QY	STANDARD;	PRT;	289 AA.	
QY	01-MAR-1992 (Rel. 21, Created)			
QY	15-DEC-1998 (Rel. 37, Last sequence update)			
QY	28-FEB-2003 (Rel. 41, Last annotation update)			
QY	Ribosome-inactivating protein karasurin precursor (rRNA			
QY	N-glycosidase) (EC 3.2.2.22).			
QY	Trichosanthes kirilowii (Mongolian snake-gourd).			
QY	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
QY	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
QY	eucotyledons I; Cucurbitales; Cucurbitaceae; Trichosanth.			
QY	NCBI_TaxID=3677;			
QY	SEQUENCE FROM N.A.			
QY	TISSUE=Root tuber;			
QY	MEDLINE=97356562; PubMed=9212998;			
QY	Mizukami H., Iida K., Kondo T., Ogiwara Y.;			
QY	"Cloning and bacterial expression of a gene encoding ribosome-			
QY	inactivating proteins, karasurin-A and karasurin-C, from Trichosanth			
QY	Kirilowii var. japonica."			
QY	Biol. Pharm. Bull. 20:711-713 (1997).			
QY	[2]			
QY	SEQUENCE OF 24-270.			
QY	MEDLINE=92005921; PubMed=1914000;			